

QY 121 GGCACGCTCTTAAGCTGCTCATTACTGCGCATCTACCCGGGAATCCGGGCTCCCTGAC 180
Db 121 GGCACGCTCTCTTAAGCTGCTCATTACTGCGCATCTACCCGGGAATCCGGGCTCCCTGAC 180
QY 181 CGATTGAGTGGGCGGGGCTGGGAGAGATTCTACTCTGACATCCGATGAGCTCTACCAACT 240
Db 181 CGATTGAGTGGGCGGGGCTGGGAGAGATTCTACTCTGACATCCGATGAGCTCTACCAACT 240
QY 241 GAAAGATTGCAACTTACTACTGTCAGCAGAGTTAGACATCCCGTACACTTTTGGCCAG 300
Db 241 GAAAGATTGCAACTTACTACTGTCAGCAGAGTTAGACATCCCGTACACTTTTGGCCAG 300
QY 301 GGGACCAAGCTGGAGATCAAA 321
Db 301 GGGACCAAGCTGGAGATCAAA 321

RESULT 2
AX003761 321 bp DNA linear PAT 24-AUG-2000
LOCUS AX003761
DEFINITION Sequence 55 from Patent WO925818.
ACCESSION AX003761
VERSION AX003761.1 GI:9227567
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Kufer, P. and Raum, T.
TITLE Method of identifying binding site domains that retain the capacity
JOURNAL Patent: WO 925818-A 55 27-MAY-1999;
KUFER PETER (DE); RAUM TOBIAS (DE)
FEATURES
source 1..321
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 98.5%; Score 316.2; DB 6; Length 321;
Best Local Similarity 99.1%; Pred. No. 3.7e-91;
Matches 318; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTGCTTCTGTGGAGACAGAGTCAAC 60
Db 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTGCTTCTGTGGAGACAGAGTCAAC 60
QY 61 ATCACTTGTGGAGCAAGTCAAGCATTTAGCACTATTAAATTGGTATCAGAGAAACCA 120
Db 61 ATCACTTGTGGAGCAAGTCAAGCATTTAGCACTATTAAATTGGTATCAGAGAAACCA 120
QY 121 GGCAGCCTCTTAAGCTGCTCATTACTGCGCATCTACCCGGGAATCCGGGCTCCCTGAC 180
Db 121 GGCAGCCTCTTAAGCTGCTCATTACTGCGCATCTACCCGGGAATCCGGGCTCCCTGAC 180
QY 181 CGATTGAGTGGGCGGGGCTGGGAGAGATTCTACTCTGACATCCGATGAGCTCTACCAACT 240
Db 181 CGATTGAGTGGGCGGGGCTGGGAGAGATTCTACTCTGACATCCGATGAGCTCTACCAACT 240
QY 241 GAAAGATTGCAACTTACTACTGTCAGCAGAGTTAGACATCCCGTACACTTTTGGCCAG 300
Db 241 GAAAGATTGCAACTTACTACTGTCAGCAGAGTTAGACATCCCGTACACTTTTGGCCAG 300
QY 301 GGGACCAAGCTGGAGATCAAA 321
Db 301 GGGACCAAGCTGGAGATCAAA 321

RESULT 3
BD075293
BD075293

LOCUS BD075293 321 bp DNA linear PAT 27-AUG-2002
DEFINITION Novel method for the production of anti-human antigen receptors and
uses thereof.
ACCESSION BD075293
VERSION BD075293.1 GI:22620896
KEYWORDS JP 2001519824-A/22.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Kufer, P. and Raum, T.
TITLE Novel method for the production of anti-human antigen receptors and
uses thereof
JOURNAL Patent: JP 2001519824-A 22 23-OCT-2001;
MICROMET AG
COMMENT OS Homo sapiens (human)
PN JP 2001519824-A/22
PD 23-OCT-2001
PF 14-APR-1998 JP 1998543494
PR 14-APR-1997 EP 97106109.8
PI PETER KUFER, TOBIAS RAUM
PC C07K16/00, C07K16/30, A61K39/395
CC Novel method for the production of anti-human antigen CC
receptors and uses
CC thereof
FH Key
FT CDS Location/Qualifiers
1..321
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 98.5%; Score 316.2; DB 6; Length 321;
Best Local Similarity 99.1%; Pred. No. 3.7e-91;
Matches 318; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTGCTTCTGTGGAGACAGAGTCAAC 60
Db 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTGCTTCTGTGGAGACAGAGTCAAC 60
QY 61 ATCACTTGTGGAGCAAGTCAAGCATTTAGCACTATTAAATTGGTATCAGAGAAACCA 120
Db 61 ATCACTTGTGGAGCAAGTCAAGCATTTAGCACTATTAAATTGGTATCAGAGAAACCA 120
QY 121 GGCAGCCTCTTAAGCTGCTCATTACTGCGCATCTACCCGGGAATCCGGGCTCCCTGAC 180
Db 121 GGCAGCCTCTTAAGCTGCTCATTACTGCGCATCTACCCGGGAATCCGGGCTCCCTGAC 180
QY 181 CGATTGAGTGGGCGGGGCTGGGAGAGATTCTACTCTGACATCCGATGAGCTCTACCAACT 240
Db 181 CGATTGAGTGGGCGGGGCTGGGAGAGATTCTACTCTGACATCCGATGAGCTCTACCAACT 240
QY 241 GAAAGATTGCAACTTACTACTGTCAGCAGAGTTAGACATCCCGTACACTTTTGGCCAG 300
Db 241 GAAAGATTGCAACTTACTACTGTCAGCAGAGTTAGACATCCCGTACACTTTTGGCCAG 300
QY 301 GGGACCAAGCTGGAGATCAAA 321
Db 301 GGGACCAAGCTGGAGATCAAA 321

RESULT 4
BD139668
BD139668
LOCUS BD139668 321 bp DNA linear PAT 18-SEP-2002
DEFINITION A novel method of identifying binding site domains that retain the
capacity of binding to an epitope.
ACCESSION BD139668
VERSION BD139668.1 GI:23234613
KEYWORDS JP 2002508924-A/53.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 321)
AUTHORS Kufer, P., Raum, T., Borschert, K., Zettl, F. and Lutterbuese, R.
TITLE A novel method of identifying binding site domains that retain the
capacity of binding to an epitope
JOURNAL Patent: JP 2002508924-A 53 26-MAR-2002;
PETER KUFER
COMMENT OS Homo sapiens (human)
PN JP 2002508924-A/53
PD 26-MAR-2002
PF 16-NOV-1998 JP 2000521184
PR 17-NOV-1997 EP 97120096.9
PI PETER KUFER, TOBIAS RAUM, KATRIN BORSCHERT, FLORIAN ZETTL, RALF
LUTTERBUESE
PC C12N15/09, A61K38/00, A61K38/22, A61K38/43, A61K39/395, C07K14/705,
C07K16/30,
PC C12N1/21, C12N5/10, C12P21/02, C12P21/08, G01N33/566, C12N15/00, PC
A61K37/02,
PC A61K37/24, A61K37/48, C12N5/00
CC A novel method of identifying binding site
domains that retain
the
CC capacity of binding to an epitope
FH Key Location/Qualifiers
FT source 1..321
FT Location/Qualifiers
1..321
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 98.5%; Score 316.2; DB 6; Length 321;
Best Local Similarity 99.1%; Pred. No. 3.7e-91;
Matches 318; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCTGCTGCTTGTGGAGACAGAGTCACC 60
DB 1 GAGCTCCAGATGACCCAGTCTCCATCTCTGCTGCTTGTGGAGACAGAGTCACC 60
QY 61 ATCACTTGTGCGACAGATGACAGATTTAAATTGATATGACAGAAACCA 120
DB 61 ATCACTTGTGCGACAGATGACAGATTTAAATTGATATGACAGAAACCA 120
QY 121 GGACAGCCCTCTAAGCTGCTCATTTAAGTGGAGATCCCGGGATCCCTGAC 180
DB 121 GGACAGCCCTCTAAGCTGCTCATTTAAGTGGAGATCCCGGGATCCCTGAC 180
QY 181 CGATTGAGTGGACGGGGTCTGGAGACAGATTTCACTCTACATGACAGTCAACCT 240
DB 181 CGATTGAGTGGACGGGGTCTGGAGACAGATTTCACTCTACATGACAGTCAACCT 240
QY 241 GAAGATTCTGCAACTTACTTCTGACAGAGTTAGACATCCCGTACCTTTGGCCAG 300
DB 241 GAAGATTCTGCAACTTACTTCTGACAGAGTTAGACATCCCGTACCTTTGGCCAG 300
QY 301 GGGACCAAGCTGGAGATCAA 321
DB 301 GGGACCAAGCTGGAGATCAA 321

RESULT 5
A84380 321 bp DNA linear PAT 21-JAN-2000
LOCUS A84380
DEFINITION Sequence 147 from Patent WO9846645.
ACCESSION A84380
VERSION A84380.1 GI:6733303
KEYWORDS
SOURCE unidentified
ORGANISM unidentified

unclassified.
REFERENCE 1 (bases 1 to 321)
AUTHORS Kufer, P. and Raum, T.
TITLE NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN RECEPTORS AND
USING THEREOF
JOURNAL Patent: WO 9846645-A 147 22-OCT-1998;
KUFER PETER (DE); RAUM TOBIAS (DE)
COMMENT OS Homo sapiens (human)
PN JP 2001519824-A/25
PD 23-OCT-2001
PF 14-APR-1998 JP 1998543494

ORIGIN
Query Match 79.6%; Score 255.4; DB 6; Length 321;
Best Local Similarity 87.2%; Pred. No. 2e-71;
Matches 280; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCTGCTGCTTGTGGAGACAGAGTCACC 60
DB 1 GAGCTCCAGATGACCCAGTCTCCATCTCTGCTGCTTGTGGAGACAGAGTCACC 60
QY 61 ATCACTTGTGCGACAGATGACAGATTTAAATTGATATGACAGAAACCA 120
DB 61 ATCACTTGTGCGACAGATGACAGATTTAAATTGATATGACAGAAACCA 120
QY 121 GGACAGCCCTCTAAGCTGCTCATTTAAGTGGAGATCCCGGGATCCCTGAC 180
DB 121 GGACAGCCCTCTAAGCTGCTCATTTAAGTGGAGATCCCGGGATCCCTGAC 180
QY 181 CGATTGAGTGGACGGGGTCTGGAGACAGATTTCACTCTACATGACAGTCAACCT 240
DB 181 CGATTGAGTGGACGGGGTCTGGAGACAGATTTCACTCTACATGACAGTCAACCT 240
QY 241 GAAGATTCTGCAACTTACTTCTGACAGAGTTAGACATCCCGTACCTTTGGCCAG 300
DB 241 GAAGATTCTGCAACTTACTTCTGACAGAGTTAGACATCCCGTACCTTTGGCCAG 300
QY 301 GGGACCAAGCTGGAGATCAA 321
DB 301 GGGACCAAGCTGGAGATCAA 321

RESULT 6
BD075296 321 bp DNA linear PAT 27-AUG-2002
LOCUS BD075296
DEFINITION Novel method for the production of anti-human antigen receptors and
uses thereof.
ACCESSION BD075296
VERSION BD075296.1 GI:22620899
KEYWORDS JP 2001519824-A/25.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 321)
AUTHORS Kufer, P. and Raum, T.
TITLE Novel method for the production of anti-human antigen receptors and
uses thereof
JOURNAL Patent: JP 2001519824-A 25 23-OCT-2001;
MICROMET AG
COMMENT OS Homo sapiens (human)
PN JP 2001519824-A/25
PD 23-OCT-2001
PF 14-APR-1998 JP 1998543494

PR	14-APR-1997	EP	97106109.8	
PI	PETER KUFER, TORIAS RAHM			
PC	C07K16/00,C07K16/30,A61K39/395			
CC	Novel method for the production of anti-human antigen CC receptors and uses thereof			
CC	thereof			
FH	Key	Location/Qualifiers		
FT	CDS	(1)..(321).		
FEATURES	source	Location/Qualifiers		
		1..321		
		/organism="Homo sapiens"		
		/mol_type="genomic DNA"		
		/db_xref="taxon:9606"		
ORIGIN				
Query Match	79.6%;	Score 255.4;	DB 6;	Length 321;
Best Local Similarity	87.2%;	Pred. No.2e-71;		
Matches	280;	Conservative	0;	Mismatches 41; Indels 0; Gaps 0;
QY	1	GAGCTCCAGATGACCCAGATCTCCATCTCCCTGCTGCTTCTGTGGAGACAGATGCACC	60	
Db	1	GAGCTCCAGATGACCCAGATCTCCATCTCCCTGCTGCTTCTGTGGAGACAGATGCACC	60	
QY	61	ATCACTTGTCCGACAGATCAGAGCATTTAGCAGCTTTTAAATTGGTATCAGAGAAACA	120	
Db	61	ATCACTTGTCCGAGGAGATCAGAGCATTTAGCAGCTTTTAAATTGGTATCAGAGAAACA	120	
QY	121	GGACAGCCTCCCTAAGCTGCTCATTTACTAGTGGCATCTACCCGGGAATCCGGGGTCCCTGAC	180	
Db	121	GGACAGCCTCCCTAAGCTGCTCATTTACTAGTGGCATCTACCCGGGAATCCGGGGTCCCTGAC	180	
QY	181	CGATTCAATGGGACGGGGTCTGGGACAGATTTCACTTCACCATCAGACAGTCTCAACCT	240	
Db	181	CGATTCAACGGGACGAGTAATCTGGGCAAAATTACACTCTCACCATCAGACAGCTCGAGCCT	240	
QY	241	GAAGATTCGCACTTACTACTGTGAGAGAGTTACGACATCCGGTACATTTGGCCAG	300	
Db	241	GAAGATTTTGCATCTACTTTTGTCAACAGTCTGACAGTTGCGGATCACCTTGCCCAA	300	
QY	301	GGGACCAAGCTGGAGATCAAA	321	
Db	301	GGGACAGCACTGGACATTCAA	321	
RESULT 7				
BD222938				
LOCUS	BD222938	1630 bp	DNA	linear
DEFINITION	Heteromimbodies.			
ACCESSION	BD222938			
VERSION	BD222938.1	GI:33032708		
KEYWORDS	JP 2002521053-A/32.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1630)			
REFERENCE	Kufner,P., Drieler,T., Baeuerle,P.A., Borschert,K. and Zettl,F. Heteromimbodies			
AUTHORS	Patent: JP 2002521053-A 32 16-JUL-2002;			
TITLE	MICROMET AG			
JOURNAL	OS Homo sapiens (human)			
COMMENT	OS Mus musculus (mouse)			
	PN JP 2002521053-A/32			
	PD 16-JUL-2002			
	PF 28-JUL-1999 JP 2000562401			
	PR 28-JUL-1998 EP 98114082.5			
	PI PETER KUFER, TORSTEN DRIELER, PATRICK A BAEUERLE, KATRIN BORSCHERT,			
	PC FLORIAN ZETTL			
	PC C12N15/09,A61K35/76,A61K38/00,A61K38/21,A61P35/00,A61P35/02,			
	PC C07K19/00,			
	PC C12N5/10,C12P21/02,G01N33/53,G01N33/53//C12N5/10,C12R1:91),			
	PC (C12P21/02,C12R1:91),C12N15/00,C12N5/00,A61K37/02,A61K37/66,			

FEATURES	source	Location/Qualifiers
PC	(C12N5/00, C12R1.91)	
CC	Heteromniobodies	
PH	Key	Location/Qualifiers
FT	CDS	(39) . (1607) .
ORIGIN		
		1. .1630
		/organism="Homo sapiens"
		/mol_type="genomic DNA"
		/db_xref="taxon:9606"
Query Match	79.6%;	Score 255.4; DB 6; Length 1630;
Best Local Similarity	87.2%;	Pred. No. 2.1e-71;
Matches 280;	Conservative 0;	Mismatches 41; Indels 0; Gaps 0
QY	1	GAGCTTCAGATGACCCAGTCTCCATCCGCCGTCTCTCTGCGGAGACAGACTCACC 60
DB	96	GAGCTTCAGATGACCCAGTCTCCATCCGCCGTCTCTCTGCGGAGACAGACTCACC 155
QY	61	ATCATCTTGTGACACAGTCCAGAGCTATTAGACTATTAAATTTGATCAGAGAAACCA 120
DB	156	ATCATCTTGTGACACAGTCCAGAGCTATTAGACTATTAAATTTGATCAGAGAAACCA 215
QY	121	GGACAGCTCTCTAGCTCTCTATTACTTGTGCGATTTACCCGGGAATCCGGGCTCCCTGAC 180
DB	216	GGACAGCTCTCTAGCTCTCTATTACTTGTGCGATTTACCCGGGAATCCGGGCTCCCTGAC 275
QY	181	CGATTCAAGTGGCAGCGGGTCTGTGGACAGATTTCACCTTCACCATCAGACAGTCTACACCT 240
DB	276	CGATTCAAGTGGCAGCGGGTCTGTGGACAGATTTCACCTTCACCATCAGACAGTCTACACCT 335
QY	241	GAAATTTCTGCACTTACTTACTGTCTGACAGAGTTACGACATCCGGTACACTTTTGGCCAG 300
DB	336	GAAATTTCTGCACTTACTTACTGTCTGACAGAGTTACGACATCCGGTACACTTTTGGCCAG 395
QY	301	GGGACCAAGCTGAGATCAAA 321
DB	396	GGGACCAAGCTGAGATCAAA 416
RESULT 8		
BD222939		
LOCUS	BD222939	1630 bp DNA linear PAT 17-JUL-2002
DEFINITION	Heteromniobodies.	
ACCESSION	BD222939	
VERSION	BD222939.1	GI:33032709
KEYWORDS	JP 2002521053-A/33.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
TITLE	Kuifer, P., Dreier, T., Baeuerle, P.A., Borschert, K. and Zettl, F.	
JOURNAL	Heteromniobodies	
COMMENT	Patent: JP 2002521053-A 33 16-JUL-2002;	
	MICROWET AG	
OS	Homo sapiens (human)	
PN	Mus musculus (mouse)	
PD	JP 2002521053-A/33	
PF	16-JUL-2002	
PI	28-JUL-1999 JP 2000562401	
PI	PETER KUPFER, TORSTEN DREIER, PATRICK A BAEUERLE, KATRIN	
BORSCHERT,		
PI	FLORIAN ZETTL	
PC	C12N15/09, A61K35/76, A61K38/00, A61K38/21, A61P35/00, A61P35/02,	
PC	C07K19/00,	
PC	C12N5/10, C12P21/02, G01N33/53, G01N33/53// (C12N5/10, C12R1.91),	
PC	(C12P21/02, C12R1.91), C12N15/00, C12N5/00, A61K37/02, A61K37/66,	
CC	C12N5/00, C12R1.91	
CC	Heteromniobodies	
PH	Key	Location/Qualifiers
FT	CDS	(39) . (1610) .

FEATURES
source
Location/Qualifiers
1..1630
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 79.6%; Score 255.4; DB 6; Length 1630;
Best Local Similarity 87.2%; Pred. No. 2.1e-71;
Matches 280; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 1 GAGCTCAGATGACCCAGTCTCATCTCCCTGCTGCTTCTGTTGGAGACAGAGTCACC 60
DB 96 GAGCTCAGATGACCCAGTCTCATCTCCCTGCTGCTTCTGTTGGAGACAGAGTCACC 155
QY 61 ATCACTTGCAGACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 120
DB 156 ATCACTTGCAGACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 215
QY 121 GGAACAGCTCTTAAGTCTGCTCACTTCACTGAGATCAACCGGAAATCCGGGGTCCCTGAC 180
DB 216 GGAACAGCTCTTAAGTCTGCTCACTTCACTGAGATCAACCGGAAATCCGGGGTCCCTGAC 275
QY 181 CGATTAGTGGCAGCGGGTCTGAGACAGATTCATCTCAGATCAAGTCAAGTCAAGTCA 240
DB 276 CGATTAGTGGCAGCGGGTCTGAGACAGATTCATCTCAGATCAAGTCAAGTCAAGTCA 335
QY 241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
DB 336 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 395
QY 301 GGGACCAAGCTGGAGATCAAA 321
DB 396 GGGACCAAGCTGGAGATCAAA 416

RESULT 9
AX023365
LOCUS AX023365 1630 bp DNA linear PAT 15-SEP-2000
DEFINITION Sequence 36 from Patent WO0006605.
ACCESSION AX023365
VERSION AX023365.1 GI:10183777
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Kufer, P., Zettl, F., Dreier, T., Baeuerle, P. A. and Borschert, K.
AUTHORS Heteromimibodies
TITLE Patent: WO 0006605-A 36 10-FEB-2000;
JOURNAL KUFER PETER (DE) ; ZETTL FLORIAN (DE) ; DREIER TORSTEN (DE) ;
BAEUEERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GES FUER
BIOMEDIZINIS (DE)
Location/Qualifiers
1..1630
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
39..1610
/note="unnamed protein product"

CDS
/codon_start=1
/protein_id="CAC08835.1"
/db_xref="GI:10183778"
/translation="MGMSCTILFLVATATGSHLQMTQSPSSLSASVGRVYTTCRA
SOSISYLMWYQKQPPKLLIYMASTRSEGVPRPSSSESTNTTLTSSIQPDP
ATYFCQSDSLPTTGQGRLLDIQGGGSGGGSGGGSEVOLLEGGGVQPGRLR
LSCASGTFSSYGMHWKQAPKGLBWAIVSYDSNRYADSVGRFTISDNKN
TLTLQNNSLRADLTVYVYCAKMGWGSWMPYIYGDWVGQGTIVTSVSGPLGDTT
HRTVAPEVFIPEPDBOLKSGTASVCLANNFYPRBAKVOIKVNALQSGNSQSV
TTQDSKDSYVLSITLTSKADYBKHKVYACVTHQGLSSPVTKSPNREGSGGGSAP
ARSPSTQPEWENNAIOEARLLINSRDPAAMNEVEVISEPDLQEPCTQCTLE
LYNGLRGSLTKLKGPLTMAASHYKHCHPPTPTSCATQITTFESTREKNKDLVLVIF

ORIGIN
FCWBPVQEHNNHHH"

Query Match 79.6%; Score 255.4; DB 6; Length 1630;
Best Local Similarity 87.2%; Pred. No. 2.1e-71;
Matches 280; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 1 GAGCTCAGATGACCCAGTCTCATCTCCCTGCTGCTTCTGTTGGAGACAGAGTCACC 60
DB 96 GAGCTCAGATGACCCAGTCTCATCTCCCTGCTGCTTCTGTTGGAGACAGAGTCACC 155
QY 61 ATCACTTGCAGACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 120
DB 156 ATCACTTGCAGACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 215
QY 121 GGAACAGCTCTTAAGTCTGCTCACTTCACTGAGATCAACCGGAAATCCGGGGTCCCTGAC 180
DB 216 GGAACAGCTCTTAAGTCTGCTCACTTCACTGAGATCAACCGGAAATCCGGGGTCCCTGAC 275
QY 181 CGATTAGTGGCAGCGGGTCTGAGACAGATTCATCTCAGATCAAGTCAAGTCAAGTCA 240
DB 276 CGATTAGTGGCAGCGGGTCTGAGACAGATTCATCTCAGATCAAGTCAAGTCAAGTCA 335
QY 241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
DB 336 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 395
QY 301 GGGACCAAGCTGGAGATCAAA 321
DB 396 GGGACCAAGCTGGAGATCAAA 416

RESULT 10
AX023367
LOCUS AX023367 1630 bp DNA linear PAT 15-SEP-2000
DEFINITION Sequence 38 from Patent WO0006605.
ACCESSION AX023367
VERSION AX023367.1 GI:10183779
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Kufer, P., Zettl, F., Dreier, T., Baeuerle, P. A. and Borschert, K.
AUTHORS Heteromimibodies
TITLE Patent: WO 0006605-A 38 10-FEB-2000;
JOURNAL KUFER PETER (DE) ; ZETTL FLORIAN (DE) ; DREIER TORSTEN (DE) ;
BAEUEERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GES FUER
BIOMEDIZINIS (DE)
Location/Qualifiers
1..1630
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
39..1613
/note="unnamed protein product"

CDS
/codon_start=1
/protein_id="CAC08836.1"
/db_xref="GI:10183780"
/translation="MGMSCTILFLVATATGSHLQMTQSPSSLSASVGRVYTTCRA
SOSISYLMWYQKQPPKLLIYMASTRSEGVPRPSSSESTNTTLTSSIQPDP
ATYFCQSDSLPTTGQGRLLDIQGGGSGGGSGGGSEVOLLEGGGVQPGRLR
LSCASGTFSSYGMHWKQAPKGLBWAIVSYDSNRYADSVGRFTISDNKN
TLTLQNNSLRADLTVYVYCAKMGWGSWMPYIYGDWVGQGTIVTSVSGPLGDTT
HRTVAPEVFIPEPDBOLKSGTASVCLANNFYPRBAKVOIKVNALQSGNSQSV
TTQDSKDSYVLSITLTSKADYBKHKVYACVTHQGLSSPVTKSPNREGSGGGSAP
ARSPSTQPEWENNAIOEARLLINSRDPAAMNEVEVISEPDLQEPCTQCTLE
LYNGLRGSLTKLKGPLTMAASHYKHCHPPTPTSCATQITTFESTREKNKDLVLVIF
LNRWTFQCSIIITLT"

ORIGIN
Query Match 79.6%; Score 255.4; DB 6; Length 1630;

Best Local Similarity 87.2%; Pred. No. 2.1e-71;
Matches 280; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTCTGCTTCTGTGGAGACAGAGTACC 60
Db 96 GAGCTCCAGATGACCCAGTCTCCATCTCCCTCTGCTTCTGTGGAGACAGAGTACC 155
QY 61 ATCACTTGTGGACAGTCAAGCATTAGAGCTTAAATTGGTATCAGCAAAACCA 120
Db 156 ATCACTTGTGGACAGTCAAGCATTAGAGCTTAAATTGGTATCAGCAAAACCA 215
QY 121 GGACAGCTCTTAAGTGTGCTATTACTGGCAGATCAACCGGAGATCCGGGGTCCCTGAC 180
Db 216 GGACAGCTCTTAAGTGTGCTATTACTGGCAGATCAACCGGAGATCCGGGGTCCCTGAC 275
QY 181 CGATTCACTGAGGAGCGGGTCTGGGACAGATTCTCACTCAACATCAGAGTCAACCT 240
Db 276 CGATTCACTGAGGAGCGGGTCTGGGACAGATTCTCACTCAACATCAGAGTCAACCT 335
QY 241 GAAGATTCTGCAACTTACTGTCAGCAGAGTACAGATCCCGTACACTTTGGCCAG 300
Db 336 GAAGATTCTGCAACTTACTGTCAGCAGAGTACAGATCCCGTACACTTTGGCCAG 395
QY 301 GGGACCAAGCTGGAGATCAA 321
Db 396 GGGACCAAGCTGGAGATCAA 416

RESULT 11
AB063929 324 bp mRNA linear PRI 02-JUL-2002
LOCUS Homo sapiens IGH mRNA for immunoglobulin kappa light chain VLJ
DEFINITION
ACCESSION AB063929
VERSION AB063929.1 GI:21669064
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hiroo, Y., Kakita, M.,
Suzuki, K., Torii, H., Urai, Y., Honda, T., Katsumi, H., Okada, J.,
Miura, K. and Kurosawa, Y.
Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics
Unpublished
2 (bases 1 to 324)
Kurosawa, Y.
Direct Submission
Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyoke 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL: http://www.fujita-hu.ac.jp/immunity/.

COMMENT
FEATURES
source
1. .324
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="K102"
/clone_1ib="AIMS4"
/note="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
1. .324
/gene="IGH"
<1. .>324
/gene="IGH"
/codon_start=1
/product="immunoglobulin kappa light chain VLJ region"
/protein_id="BAC01557.1"

ORIGIN

Query Match 77.6%; Score 249; DB 9; Length 324;
Best Local Similarity 86.0%; Pred. No. 2.3e-69;

Matches 276; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTCTGCTTCTGTGGAGACAGAGTACC 60
Db 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTCTGCTTCTGTGGAGACAGAGTACC 60
QY 61 ATCACTTGTGGACAGTCAAGCATTAGAGCTTAAATTGGTATCAGCAAAACCA 120
Db 61 ATCACTTGTGGACAGTCAAGCATTAGAGCTTAAATTGGTATCAGCAAAACCA 120
QY 121 GGACAGCTCTTAAGTGTGCTATTACTGGCAGATCAACCGGAGATCCGGGGTCCCTGAC 180
Db 121 GGACAGCTCTTAAGTGTGCTATTACTGGCAGATCAACCGGAGATCCGGGGTCCCTGAC 180
QY 181 CGATTCACTGAGGAGCGGGTCTGGGACAGATTCTCACTCAACATCAGAGTCAACCT 240
Db 181 AGTTCACTGAGGAGCGGGTCTGGGACAGATTCTCACTCAACATCAGAGTCAACCT 240
QY 241 GAAGATTCTGCAACTTACTGTCAGCAGAGTACAGATCCCGTACACTTTGGCCAG 300
Db 241 GAAGATTCTGCAACTTACTGTCAGCAGAGTACAGATCCCGTACACTTTGGCCAG 300
QY 301 GGGACCAAGCTGGAGATCAA 321
Db 301 GGGACCAAGCTGGAGATCAA 321

RESULT 12
AB064098 828 bp mRNA linear PRI 02-JUL-2002
LOCUS Homo sapiens IGH mRNA for immunoglobulin kappa light chain VLJ
DEFINITION
ACCESSION AB064098
VERSION AB064098.1 GI:21669402
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hiroo, Y., Kakita, M.,
Suzuki, K., Torii, H., Urai, Y., Honda, T., Katsumi, H., Okada, J.,
Miura, K. and Kurosawa, Y.
Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics
Unpublished
2 (bases 1 to 828)
Kurosawa, Y.
Direct Submission
Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyoke 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL: http://www.fujita-hu.ac.jp/immunity/.

COMMENT
FEATURES
source
1. .828
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="K57"
/clone_1ib="AIMS4"
/note="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"

gene 1..828
/gene="IGK"
CDS 1..828
/gene="IGK"
/codon_start=1
/product="immunoglobulin kappa light chain VJL region"
/protein_id="BAC01726.1"
/db_xref="GI:2169403"
/translation="MKYLLPTAAAGLLLLAQAQPMADIQMTQSPSSLSASVGRVTIT
CRASQSISSSLYMWYQQKPGKAPKLLIYAASLSQGVSPFSGSGSDTFTLTSLIQP
EDPATYVCOOSYPTFGSGTLEIKRTVAAPSVPFPSPDQLKSGTASVCLIN
FYPRAKYNQWKYDNLQSGNSQSTVEDQSDTSLTSLTSLKADYKHKYAAEV
THQGLSSPTKSFNKGECASARQSTPFVCRVQGSQSLPPPPNAGGSGSGSGSGS

sig_peptide 1..66
/gene="IGK"
/note="pe1B signal peptide"

ORIGIN

Query Match 77.6%; Score 249; DB 9; Length 828;
Best Local Similarity 86.0%; Pred. No. 2.4e-69;
Matches 276; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GAGCTCAGATGACCCAGTCTCATCTCCCTGCTTCTGTGGAGACAGAGTCACC 60
|||
DB 67 GACATCAATGACCCAGTCTCATCTCCCTGCTTCTGTGGAGACAGAGTCACC 126
|||
QY 61 ATCACTTGTGCAAGTCAAGACATTTAGCAGCTATTAAATTGTATCAGAGAAACCA 120
|||
DB 127 ATCACTTGTGCGGCAAGTCAAGACATTTAGCAGCTATTAAATTGTATCAGAGAAACCA 186
|||
QY 121 GGAACAGCTTCTTAAGTCTCATTTACTGGCGATTCACCCGGAATCCGGGCTCCTGAC 180
|||
DB 187 GGGAAAGCCCTTAAGTCTCATTTACTGGCGATTCACCCGGAATCCGGGCTCCTGAC 246
|||
QY 181 CGATTGAGTGGAGCGGGTCTGGAGACAGATTTCATCTCAACATCCGATCAACAACCT 240
|||
DB 247 AGGTTAGTGGAGCGGGTCTGGAGACAGATTTCATCTCAACATCCGATCAACAACCT 306
|||
QY 241 GAAGATTTCGCAACTTACTACTGTCAAGAGATTAGACATCCCGTACACTTTTGGCCAG 300
|||
DB 307 GAAGATTTCGCAACTTACTACTGTCAAGAGATTAGACATCCCGTACACTTTTGGCCAG 366
|||
QY 301 GGGACCAAGCTGGAGATCAAA 321
|||
DB 367 GGGACCAAGCTGGAGATCAAA 387
|||

RESULT 13
E12913
LOCUS E12913 321 bp DNA linear PAT 27-APR-1998
DEFINITION Human cDNA encoding variable region of light chain anti-pulmonary
carcinoma monoclonal antibody.
ACCESSION E12913
VERSION E12913.1 GI:3251744
KEYWORDS JP 1997098786-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 321)
Shitahata,S., Mochizuki,K. and Kato,M.
ANTIBODY CDNA
Patent: JP 1997098786-A 2 15-APR-1997;
MORINAGA & CO LTD, RES DEV CORP OF JAPAN
OS Homo sapiens (human)
PN JP 1997098786-A/2
PD 15-APR-1997
PF 06-OCT-1995 JP 1995284400
PI SHIRAHATA SANETAKA, MOCHIZUKI KATSUMI, KATO MASATOSHI PC
C12N15/09,C07H21/04,C07K16/32,C12P21/08//C12N5/10,C12P21/08, PC
C12R1:91),
PC (C12N5/10,C12R1:91);

CC strandedness: Double;
CC topology: Linear;
FH key Location/Qualifiers
FT source 1..321
FT /organism="Homo sapiens"
FT /cell_type="hybridoma cell",
FT /cell_line="AE-6"
FT mat_peptide 1..321
FT /product="variable region of light chain
anti-pulmonary
carcinoma monoclonal antibody" FT
FT misc_feature 70..102
FT /note="this region encodes Complementarity
determining
region (CDR-1)"
FT misc_feature 148..168
FT /note="this region encodes Complementarity
determining
region (CDR-2)"
FT misc_feature 265..291
FT /note="this region encodes Complementarity
determining
region (CDR-3)"
FT Location/Qualifiers
FT source 1..321
FT /organism="Homo sapiens"
FT /mol_type="genomic DNA"
FT /db_xref="taxon:9606"

ORIGIN

Query Match 76.6%; Score 245.8; DB 6; Length 321;
Best Local Similarity 85.4%; Pred. No. 2.6e-68;
Matches 274; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 GAGCTCAGATGACCCAGTCTCATCTCCCTGCTTCTGTGGAGACAGAGTCACC 60
|||
DB 1 GACATCAATGACCCAGTCTCATCTCCCTGCTTCTGTGGAGACAGAGTCACC 60
|||
QY 61 ATCACTTGTGCAAGTCAAGACATTTAGCAGCTATTAAATTGTATCAGAGAAACCA 120
|||
DB 61 ATCACTTGTGCGGCAAGTCAAGACATTTAGCAGCTATTAAATTGTATCAGAGAAACCA 120
|||
QY 121 GGAACAGCTTCTTAAGTCTCATTTACTGGCGATTCACCCGGAATCCGGGCTCCTGAC 180
|||
DB 121 GGGAAAGCCCTTAAGTCTCATTTACTGGCGATTCACCCGGAATCCGGGCTCCTGAC 180
|||
QY 181 CGATTGAGTGGAGCGGGTCTGGAGACAGATTTCATCTCAACATCCGATCAACAACCT 240
|||
DB 181 AGGTTAGTGGAGCGGGTCTGGAGACAGATTTCATCTCAACATCCGATCAACAACCT 240
|||
QY 241 GAAGATTTCGCAACTTACTACTGTCAAGAGATTAGACATCCCGTACACTTTTGGCCAG 300
|||
DB 241 GAAGATTTCGCAACTTACTACTGTCAAGAGATTAGACATCCCGTACACTTTTGGCCAG 300
|||
QY 301 GGGACCAAGCTGGAGATCAAA 321
|||
DB 301 GGGACCAAGCTGGAGATCAAA 321
|||

RESULT 14
HUM1GKC
LOCUS HUM1GKC 324 bp mRNA linear PRI 27-JUL-1994
DEFINITION Human IgK (thyroid peroxidase-specific Fab fragment) mRNA, partial
cde.
ACCESSION L12108
VERSION L12108.1 GI:397789
KEYWORDS V-region; autoimmune; immunoglobulin kappa-chain.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 324)

AUTHORS Portolano, S., McIlachlan, S.M. and Rapoport, B.
TITLE High affinity, thyroid-specific human autoantibodies displayed on the surface of filamentous phage use V genes similar to other autoantibodies
JOURNAL J. Immunol. 151 (5), 2839-2851 (1993)
MEDLINE 93367244
PUBMED 8360495
COMMENT Original source text: Homo sapiens cDNA to mRNA.
FEATURES Location/Qualifiers
 source 1..324
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /map="2p12"
 1..324
 /gene="IGKV"
 <1..>324
 /gene="IGKV"
 /note="clone TR1.22"
 /codon_start=1
 /product="immunoglobulin kappa chain"
 /protein_id="AA020106.1"
 /db_xref="GI:397790"
 /translation="ELVMTQSPSSLSASVGVRIITCRASQSISSYLMWYQKPGTAP KLIVASTLQSGVPSRFSGSGSGTDFTLTISLQPEDPATYTCQGSYGTPTFGGT KLEIKR"
ORIGIN
 Query Match 76.6%; Score 245.8; DB 9; Length 324;
 Best Local Similarity 85.4%; Pred. No. 2.6e-68;
 Matches 274; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
 QY 1 GAGCTCAATGACCCAGTCTCATCTCCCTGCTCTGCTGTGGAGACAGAGTACC 60
 DB 1 GAGCTGTATGACCCAGTCTCATCTCCCTGCTGTGCACTGTAGAGACAGAGTACC 60
 QY 61 ATCACTTGTGCAAGTCAAGATGAGCATTAAGATTAATTTGATCAGAGAAACA 120
 DB 61 ATCACTTGTGCGGAGTCAAGATGAGCATTAAGATTAATTTGATCAGAGAAACA 120
 QY 121 GAGACAGCTCTAAGTCTCATTTAAGTGGAGATCAACCCGGGAATCCGGGTCCTGAC 180
 DB 121 GAGACAGCCCTTAAGTCTCATTTAAGTGGAGATCAACCCGGGATCCGGGTCCTGAC 180
 QY 181 CGATTCAAGTGGAGAGGGGCTGAGGAGATTTCACTCTGACATCGACATCTCAACCT 240
 DB 181 AGGTTCAAGTGGAGAGGGGCTGAGGAGATTTCACTCTGACATCGACATCTCAACCT 240
 QY 241 GAAGATTCTGCAACTACTACTGTGACAGAGATTACAGATCCGATCACTTTGGCCAG 300
 DB 241 GAAGATTCTGCAACTACTACTGTGACAGAGATTACAGATCCGATCACTTTGGCCAG 300
 QY 301 GGGACCAAGCTGAGATCAAA 321
 DB 301 GGGACCAAGCTGAGATCAAA 321
RESULT 15
AB063952
LOCUS Homo sapiens IGK mRNA for immunoglobulin kappa light chain VJ
DEFINITION Homo sapiens IGK mRNA for immunoglobulin kappa light chain VJ
AB063952
ACCESSION AB063952
VERSION AB063952.1 GI:21669110
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirose, Y., Kakita, M., Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J., Mura, K. and Kurosawa, Y.

TITLE Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional genomics
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 321)
AUTHORS Kurosawa, Y.
JOURNAL Direct Submission
 Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsukake-cho, Toyooka 470-1192, Japan
 (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT Please visit our web site
 URL: <http://www.fujita-hu.ac.jp/immunity/>.
FEATURES Location/Qualifiers
 source 1..321
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="K125"
 /clone_1b="AIMS4"
 /note="mixture of tissues: tonsils, umbilical cords, peripheral blood and bone marrow"
 1..321
 /gene="IGK"
 <1..>321
 /gene="IGK"
 /codon_start=1
 /product="immunoglobulin kappa light chain VJ region"
 /protein_id="BAC01580.1"
 /db_xref="GI:21669111"
 /translation="DIQMTQSPSSLSASIGDRVITCRASQSISSYLMWYQKPGKAP KLITVAASNLQSGVPSRFSGSGSGTDFTLTISLQPEDPATYTCQGSYNTPTFGGT KLEIKR"
ORIGIN
 Query Match 76.1%; Score 244.2; DB 9; Length 321;
 Best Local Similarity 85.0%; Pred. No. 8.5e-68;
 Matches 273; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
 QY 1 GAGCTCAATGACCCAGTCTCATCTCCCTGCTCTGCTGTGGAGACAGATCAC 60
 DB 1 GACATCCAGATGACCCAGTCTCATCTCCCTGCTGTGCTATAGAGACAGATCAC 60
 QY 61 ATCACTTGTGCAAGTCAAGATGAGCATTAAGATTAATTTGATCAGAGAAACA 120
 DB 61 ATCACTTGTGCGGAGTCAAGATGAGCATTAAGATTAATTTGATCAGAGAAACA 120
 QY 121 GAGACAGCTCTAAGTCTCATTTAAGTGGAGATCAACCCGGGAATCCGGGTCCTGAC 180
 DB 121 GGGAAAGCCCTTAAGTCTCATTTAAGTGGAGATCAACCCGGGATCCGGGTCCTGAC 180
 QY 181 CGATTCAAGTGGAGAGGGGCTGAGGAGATTTCACTCTGACATCGACATCTCAACCT 240
 DB 181 AGGTTCAAGTGGAGAGGGGCTGAGGAGATTTCACTCTGACATCGACATCTCAACCT 240
 QY 241 GAAGATTCTGCAACTACTACTGTGACAGAGATTACAGATCCGATCACTTTGGCCAG 300
 DB 241 GAAGATTCTGCAACTACTACTGTGACAGAGATTACAGATCCGATCACTTTGGCCAG 300
 QY 301 GGGACCAAGCTGAGATCAAA 321
 DB 301 GGGACCAAGCTGAGATCAAA 321

Search completed: December 7, 2004, 08:53:00
 Job time : 1817.78 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: December 6, 2004, 22:52:33 ; Search time 271.757 Seconds
(without alignments)
6200.629 Million cell updates/sec

Title: US-09-403-107-141

Perfect score: 321

Sequence: 1 gagccacagatgaccagcgc.....ggaccacagctggagatcaaa 321

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_23sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	316.2	98.5	321	2	AAV68536
2	316.2	98.5	321	2	AAV68536 Nucleotide
3	255.4	79.6	1630	3	AAV68539
4	255.4	79.6	1630	3	AAV68539 Nucleotide
5	255.4	79.6	1630	3	AAV68539 Nucleotide
6	245.8	75.6	321	2	AAV68539
7	245.8	75.6	321	2	AAV68539 Nucleotide
8	242.6	75.6	321	2	AAV68539
9	242.6	75.6	321	2	AAV68539 Nucleotide
10	242.6	75.6	321	2	AAV68539 Nucleotide
11	242.6	75.6	321	2	AAV68539 Nucleotide
12	239.2	74.5	321	2	AAV68539
13	239.2	74.5	321	2	AAV68539 Nucleotide
14	237.8	74.1	321	2	AAV68539
15	237.8	74.1	321	2	AAV68539 Nucleotide
16	237.8	74.1	321	2	AAV68539 Nucleotide
17	237.8	74.1	321	2	AAV68539 Nucleotide
18	237.8	74.1	321	2	AAV68539 Nucleotide
19	236.2	73.6	321	2	AAV68539
20	236.2	73.6	321	2	AAV68539 Nucleotide
21	236.2	73.6	321	2	AAV68539 Nucleotide

22	236.2	73.6	720	10	ABZ76706	ABZ76706 Human ser
23	236.2	73.6	720	12	ADL92368	ADL92368 Human pta
24	236.2	73.5	321	5	AAH68658	AAH68658 Human ant
25	236.2	73.5	321	5	ACD45322	ACD45322 Anti-Rh(D
26	234.6	73.1	315	2	AAV19765	AAV19765 Antibody
27	234.6	73.1	322	6	ABZ62720	ABZ62720 Anti-IGF-
28	234.6	73.1	729	3	AAH11630	AAH11630 Human imm
29	234.6	73.1	729	6	ABH46009	ABH46009 Humanised
30	233	72.6	315	2	AAV19767	AAV19767 Antibody
31	231.4	72.1	321	12	ADU93583	ADU93583 Human CD4
32	231.4	72.1	321	12	ADU93583	ADU93583 Human CD4
33	231.4	72.1	324	4	ADU93583	ADU93583 Human HIV
34	231.4	72.1	324	10	AAV52122	AAV52122 Human ant
35	231.4	72.1	1106	6	ABO54241	ABO54241 Human ova
36	231.2	72.0	321	5	AAH68654	AAH68654 Human ant
37	231.2	72.0	321	5	ACD45318	ACD45318 Anti-Rh(D
38	230	71.7	341	2	AAV60119	AAV60119 Coding se
39	229.8	71.6	315	2	AAV19761	AAV19761 Antibody
40	229.8	71.6	324	12	ADU92385	ADU92385 Anti-HSA
41	229.8	71.6	333	2	AAV79686	AAV79686 Human can
42	229.8	71.6	342	4	AAH47727	AAH47727 Nucleotide
43	229.6	71.5	321	5	AAH68720	AAH68720 Human ant
44	229.6	71.5	321	5	AAH68647	AAH68647 Human ant
45	229.6	71.5	321	9	ACD45311	ACD45311 Anti-Rh(D

ALIGNMENTS

RESULT 1	AAV68536	standard; DNA; 321 BP.
ID	AAV68536	
AC	AAV68536	
XX		
DT	16-FEB-1999	(first entry)
XX		
DE	Nucleotide sequence of human kappa 8 light chain variable region.	
XX		
KW	Human; kappa 8 light chain variable region; receptor; antigen; tumour;	
KW	auto-immune disease; graft rejection; allergy; inflammatory disease;	
KW	endocrine disease; degenerative disease; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..321
FT		/ftag= a
XX		/product= "human kappa 8 light chain variable region"
XX		
PN	WO9846645-A2.	
XX		
PD	22-OCT-1998.	
XX		
PF	14-APR-1998;	98WO-EP002180.
XX		
PR	14-APR-1997;	97EP-00106109.
XX		
PA	(KUPE/) KUFER P.	
PA	(RAUM/) RAUM T.	
XX		
PI	Kufer P, Raum T;	
XX		
DR	WPI; 1998-594564/50.	
DR	P-PSDB; AAW80814.	
XX		
PT	Production of anti-human antigen receptors - by selecting a combination	
PT	of functionally rearranged VH and VL immunoglobulin chains expressed from	
XX	a recombinant vector.	
XX		
PS	Claim 9; Fig 6; 84p; English.	
XX		
CC	This is the nucleotide sequence of the human kappa 8 light chain variable	

CC region, used in the method of the invention, for providing receptors that
CC can be used for targeting antigens in humans without being immunogenic
CC themselves. Such receptors can be used for treating diseases such as
CC tumours or auto-immune diseases, graft rejection after transplantation,
CC infectious diseases by targeting cellular receptors as well as allergic,
CC inflammatory, endocrine and degenerative diseases by targeting key
CC molecules involved in the pathological process

XX Sequence 321 BP; 81 A; 91 C; 75 G; 74 T; 0 U; 0 Other;

Query Match 98.5%; Score 316.2; DB 2; Length 321;

Best Local Similarity 99.1%; Pred. No. 2.9e-93;

Matches 318; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCTGCTGCTTCTGTGGAGACAGAGTACC 60

DB 1 GAGCTCCAGATGACCCAGTCTCCATCTCTGCTGCTTCTGTGGAGACAGAGTACC 60

QY 61 ATCACTTGTGGAGCAAGTACAGAGATTAAGATTAATTTGGTATCAGAGAAACCA 120

DB 61 ATCACTTGTGGAGCAAGTACAGAGATTAAGATTAATTTGGTATCAGAGAAACCA 120

QY 121 GGACAGCTCTCTTAAGTCTCATTTTACTGAGCATCTACCCGGGAATCCGGGGTCCCTGAC 180

DB 121 GGACAGCTCTCTTAAGTCTCATTTTACTGAGCATCTACCCGGGAATCCGGGGTCCCTGAC 180

QY 181 CGATTCAGTGGAGCGGGTCTGGAGCAGATTTCATCTCAGCATCAGAGTCAACACT 240

DB 181 CGATTCAGTGGAGCGGGTCTGGAGCAGATTTCATCTCAGCATCAGAGTCAACACT 240

QY 241 GAAGATTTGCAACTTACTGTCAGAGAGTTAGAGATCCCGACCTTTGGCCAG 300

DB 241 GAAGATTTGCAACTTACTGTCAGAGAGTTAGAGATCCCGACCTTTGGCCAG 300

QY 301 GGGACCAAGCTGGAGATCAAA 321

DB 301 GGGACCAAGCTGGAGATCAAA 321

RESULT 2
AA77237
ID AAX77237 standard; DNA; 321 BP.

XX AAX77237;

DT 04-AUG-1999 (first entry)

DE Human kappa 8 light chain variable region encoding DNA.

KW Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
KW autoimmune disease; scfv-antibody; single-chain fv; ss.

OS Homo sapiens.

PN WO925818-A1.

PD 27-MAY-1999.

PF 16-NOV-1998; 98WO-EP007313.

PR 17-NOV-1997; 97EP-00120096.

PA (KUFE/) KUFER P.

PI Kufer P, Raum T, Borschert K, Zettl F, Lutterbuese R;

XX MPI; 1999-338004/28.

DR P-PDB; AAY17955.

PT Phage display system for identification of binding site domains retaining
PT capacity to bind an epitope.

PS Disclosure; Fig 3.2; 152pp; English.

XX The invention relates to a method of identifying binding site domains
CC (BSD) that retain the capacity of binding to a predetermined epitope when
CC positioned C-terminal of at least one further domain in a recombinant bi-
CC or multivalent polypeptide. The method comprises (a) testing a panel of
CC BSD displayed on the surface of a biological display system as part of a
CC fusion protein for binding to a predetermined epitope, where the fusion
CC protein comprises an additional domain positioned N-terminal of the BSD
CC and an amino acid sequence that mediates anchoring of the fusion protein
CC to the surface of the display system; and (b) identifying a BSD that
CC binds to the predetermined epitope. The method is useful to identify bi-
CC or multivalent polypeptides that comprise antibody binding sites capable
CC of efficiently binding to the corresponding antigen. The polypeptides or
CC antibodies identified by the method are useful therapeutically and
CC fragments that bind independently of their position within bifunctional
CC single-chain fusion proteins can be isolated from combinatorial antibody
CC libraries using the new in vitro method

XX Sequence 321 BP; 81 A; 91 C; 75 G; 74 T; 0 U; 0 Other;

Query Match 98.5%; Score 316.2; DB 2; Length 321;

Best Local Similarity 99.1%; Pred. No. 2.9e-93;

Matches 318; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCTGCTGCTTCTGTGGAGACAGAGTACC 60

DB 1 GAGCTCCAGATGACCCAGTCTCCATCTCTGCTGCTTCTGTGGAGACAGAGTACC 60

QY 61 ATCACTTGTGGAGCAAGTACAGAGATTAAGATTAATTTGGTATCAGAGAAACCA 120

DB 61 ATCACTTGTGGAGCAAGTACAGAGATTAAGATTAATTTGGTATCAGAGAAACCA 120

QY 121 GGACAGCTCTCTTAAGTCTCATTTTACTGAGCATCTACCCGGGAATCCGGGGTCCCTGAC 180

DB 121 GGACAGCTCTCTTAAGTCTCATTTTACTGAGCATCTACCCGGGAATCCGGGGTCCCTGAC 180

QY 181 CGATTCAGTGGAGCGGGTCTGGAGCAGATTTCATCTCAGCATCAGAGTCAACACT 240

DB 181 CGATTCAGTGGAGCGGGTCTGGAGCAGATTTCATCTCAGCATCAGAGTCAACACT 240

QY 241 GAAGATTTGCAACTTACTGTCAGAGAGTTAGAGATCCCGACCTTTGGCCAG 300

DB 241 GAAGATTTGCAACTTACTGTCAGAGAGTTAGAGATCCCGACCTTTGGCCAG 300

QY 301 GGGACCAAGCTGGAGATCAAA 321

DB 301 GGGACCAAGCTGGAGATCAAA 321

RESULT 3
AAV68539
ID AAV68539 standard; DNA; 321 BP.

XX AAV68539;

DT 16-FEB-1999 (first entry)

DE Nucleotide sequence of human kappa 5.1 light chain variable region.

KW Human; kappa 5.1 light chain variable region; receptor; antigen; tumour;
KW auto-immune disease; graft rejection; allergy; inflammatory disease;
KW endocrine disease; degenerative disease; ss.

OS Homo sapiens.

XX Homo sapiens.

XX Key

FT CDS Location/Qualifiers

FT 1..321 /tag= a

FT /product= "human kappa 5.1 light chain variable region"

XX WO9846645-A2.

PD 22-OCT-1998.
 XX
 PF 14-APR-1998; 98WO-EP002180.
 XX
 PR 14-APR-1997; 97BP-00106109.
 XX
 PA (KUPE/) KUFER P.
 PA (RAUM/) RAUM T.
 XX
 PI Kufer P, Raum T;
 XX
 DR WPI; 1998-594564/50.
 XX
 P-PsDB; AAW68539.
 XX
 PT Production of anti-human antigen receptors - by selecting a combination
 PT of functionally rearranged VH and VL immunoglobulin chains expressed from
 PT a recombinant vector.
 XX
 PS Claim 9; Fig 9; 84pp; English.
 XX
 CC This is the nucleotide sequence of the human kappa light chain variable
 CC region, used in the method of the invention, for providing receptors that
 CC can be used for targeting antigens in humans without being immunogenic
 CC themselves. Such receptors can be used for treating diseases such as
 CC tumours or auto-immune diseases, graft rejection after transplantation,
 CC infectious diseases by targeting cellular receptors as well as allergic,
 CC inflammatory, endocrine and degenerative diseases by targeting key
 CC molecules involved in the pathological process
 XX
 SQ Sequence 321 BP; 81 A; 93 C; 72 G; 75 T; 0 U; 0 Other;
 XX
 Query Match 79.6%; Score 255.4; DB 2; Length 321;
 Best Local Similarity 87.2%; Pred. No. 2.6e-73;
 Matches 280; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
 XX
 QY 1 GAGCTCAGATGACCCAGTCTCCATCTCCCTGCTCTGTGGAGACAGATCACC 60
 DB 1 GAGCTCAGATGACCCAGTCTCCATCTCCCTGCTCTGTGGAGACAGATCACC 60
 XX
 QY 61 ATCACTTGTGGACAAGTCAGACATTAAGAGCTATTAAATTTGGATACAGAGAAACCA 120
 DB 61 ATCACTTGTGGACAAGTCAGACATTAAGAGCTATTAAATTTGGATACAGAGAAACCA 120
 XX
 QY 121 GGAACACCTCTTAAGTGTCTCATTTTCTGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
 DB 121 GGAACACCTCTTAAGTGTCTCATTTTCTGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
 XX
 QY 181 CGATTGAGTGGACGGGGTCTGGAGACAGATTTCACTCTCAGTCAGACAGTCTAACACT 240
 DB 181 CGATTGAGTGGACGGGGTCTGGAGACAGATTTCACTCTCAGTCAGACAGTCTAACACT 240
 XX
 QY 241 GAAAGATTCTGCAACTTACTGTACAGACAGATTAGACATCCCGTACACTTTTGGCCAG 300
 DB 241 GAAAGATTCTGCAACTTACTGTGCAACAGTGTGACAGAGTTGGCCGATCACTTCCGGCAA 300
 XX
 QY 301 GGGACCAAGCTGGAGATCAAA 321
 DB 301 GGGACCAAGCTGGAGATCAAA 321
 XX
 RESULT 4
 AA250588
 ID AA250588 standard; DNA; 1630 BP.
 XX
 AC AA250588;
 XX
 DT 23-MAY-2000 (first entry)
 XX
 DE HD70scFv-Ck-interleukin 2 encoding DNA.
 XX
 KW HD70; single-chain variable fragment; scFv; 17-1A antigen; human; EPCAM;
 KW epithelial cell adhesion molecule; inflammatory cytokine; IL-2;
 KW interleukin-2; Ck-domain; kappa light chain constant domain;

KW heteroninbody; multifunctional compound; immunoglobulin; cyostatic;
 KW immunostimulatory; antileukemia; diagnosis; prevention;
 KW antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;
 KW leukemia; solid tumour; carcinoma; melanoma; sarcoma; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 39..1613
 FT /tag= a
 FT /product= "HD70scFv-Ck-IL-2 chain"
 FT misc_feature 95..842
 FT /tag= b
 FT /label= HD70_scFv
 XX
 PN WO200006605-A2.
 XX
 PD 10-FEB-2000.
 XX
 PF 28-JUL-1999; 99WO-EP005416.
 XX
 PR 28-JUL-1998; 98BP-00114082.
 XX
 PA (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
 XX
 PI Kufer P, Dreier T, Baerle PA, Borsche K, Zettl F;
 XX
 DR WPI; 2000-195265/17.
 DR P-PsDB; AAY44995.
 XX
 PT New multifunctional compounds useful for preventing and/or treating
 PT malignant cell growth and for detection and diagnosis.
 XX
 PS Claim 8; Fig 55B; 166pp; English.
 XX
 CC The patent discloses heteroninbodies which are multifunctional compounds
 CC producible in a mammalian host cell as a secretable and fully functional
 CC heterodimer of two polypeptide chains, where one of the polypeptide
 CC chains comprises a CH1-domain (constant domain of an immunoglobulin
 CC heavy chain) and the other chain comprises a C_μ-domain (constant domain of
 CC an immunoglobulin light chain). The polypeptide chains further comprise,
 CC fused to the constant domains at least two (poly)peptides having
 CC different receptor or ligand functions, where further at least two of the
 CC different (poly)peptides lack an intrinsic affinity for one another and
 CC are linked via the constant domains. The heteroninbodies have
 CC cyostatic, immunostimulatory, antileukemia and antiproliferative
 CC activities. These compounds can be used for diagnosing, preventing and
 CC treating malignant cell growth related to malignancies of haematopoietic
 CC cells e.g. lymphomas and leukemias, or to solid tumours e.g. carcinomas,
 CC melanomas and sarcomas. The present sequence is a DNA encoding right
 CC chain of a heteroninbody comprising HD70 single-chain Fv (scFv) fragment
 CC N-terminally linked to human Ck domain (constant domain of immunoglobulin
 CC -kappa light chain) which bears at its C-terminus the human inflammatory
 CC cytokine interleukin-2 (IL-2). HD70 scFv specifically recognises the
 CC human epithelial cell adhesion molecule (EPCAM) also called 17-1A antigen
 XX
 SQ Sequence 1630 BP; 445 A; 410 C; 408 G; 367 T; 0 U; 0 Other;
 XX
 Query Match 79.6%; Score 255.4; DB 3; Length 1630;
 Best Local Similarity 87.2%; Pred. No. 5e-73;
 Matches 280; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
 XX
 QY 1 GAGCTCAGATGACCCAGTCTCCATCTCCCTGCTCTGTGGAGACAGATCACC 60
 DB 96 GAGCTCAGATGACCCAGTCTCCATCTCCCTGCTCTGTGGAGACAGATCACC 155
 XX
 QY 61 ATCACTTGTGGACAAGTCAGACATTAAGAGCTATTAAATTTGGATACAGAGAAACCA 120
 DB 156 ATCACTTGTGGACAAGTCAGACATTAAGAGCTATTAAATTTGGATACAGAGAAACCA 215
 XX
 QY 121 GGAACACCTCTTAAGTGTCTCATTTTCTGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
 DB 216 GGAACACCTCTTAAGTGTCTCATTTTCTGCGATCTACCCGGGAATCCGGGGTCCCTGAC 275

QY 181 CGATTTCAGTGGACGCGGTCTGGACAGATTTCACCTCTACCATCAGAGCTTACAACT 240
 DB 276 CGATTTCAGCGGACGATGAATGGACAAATTAACCTCTACCATCAGAGCTTACAACT 335
 QY 241 GAAGATTCCTGCACTTACTACTCTGACAGAGTATGACATCCGCTACCTTTGGCCAG 300
 DB 336 GAAGATTTTGTCTACTTACTTTTGTCAACAGCTGACAGTTTGGCATCCTTCGACCA 395
 QY 301 GGGACCAAGCTGGAGATCAAA 321
 DB 396 GGGACAGACTGCAGATTCAA 416

RESULT 5
 AA250587
 ID AA250587 standard; DNA, 1630 BP.
 AC AA250587;
 XX
 DT 23-MAY-2000 (first entry)
 XX
 DE HD70scFv-CH1-GM-CSF chain encoding DNA.
 XX
 KM HD70; single-chain variable fragment; scFv; 17-1A antigen; human; EPCAM;
 KM epithelial cell adhesion molecule; inflammatory cytokine; GM-CSF;
 KM granulocyte/macrophage colony stimulating factor; heteromibody;
 KM CH1-domain; multifunctional compound; heavy chain constant domain;
 KM immunoglobulin; cytoskeletal; immunostimulatory; antileukemia; diagnosis;
 KM antiproliferative; prevention; treatment; malignant; haematopoietic cell;
 KM lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 39..1610
 FT /*tag= a
 FT /product= "HD70scFv-CH1-GM-CSF chain"
 FT 96..842
 FT /*tag= b
 FT /label= HD70_scFv
 XX
 PN WO200006605-A2.
 XX
 PD 10-FEB-2000.
 XX
 PF 28-JUL-1999; 99WO-EP005416.
 XX
 PR 28-JUL-1998; 98EP-00114082.
 XX
 PA (MIGR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
 XX
 PI Kufer P, Dreier T, Baeuerle PA, Borsche K, Zettl F;
 XX MPI, 2000-195265/17.
 DR P-PSDB; AAY44994.
 DR
 XX
 XX New multifunctional compounds useful for preventing and/or treating
 PT malignant cell growth and for detection and diagnosis.
 PT
 XX
 PS Claim 8; Fig 55A; 166pp; English.
 CC
 CC The patent discloses heteromibodies which are multifunctional compounds
 CC producible in a mammalian host cell as a secretable and fully functional
 CC heterodimer of two polypeptide chains, where one of the polypeptide
 CC chains comprises a CH1-domain (constant domain of an immunoglobulin
 CC heavy chain) and the other chain comprises a CH2-domain (constant domain of
 CC an immunoglobulin light chain). The polypeptide chains further comprise,
 CC fused to the constant domains at least two (poly)peptides having
 CC different receptor or ligand functions, where further at least two of the
 CC different (poly)peptides lack an intrinsic affinity for one another and
 CC are linked via the constant domains. The heteromibodies have
 CC cytostatic, immunostimulatory, antileukemia and antiproliferative

CC activities. These compounds can be used for diagnosing, preventing and
 CC treating malignant cell growth related to malignancies of haematopoietic
 CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
 CC melanomas and sarcomas. The present sequence is a DNA encoding left chain
 CC of a heteromibody comprising HD70 single-chain Fv (scFv) fragment N-
 CC terminally linked to human CH1 domain which bears at its C-terminus the
 CC human inflammatory cytokine granulocyte/macrophage colony stimulating
 CC factor (GM-CSF), plus a hexahistidine sequence for ease of purification.
 CC HD70 scFv specifically recognises the human epithelial cell adhesion
 CC molecule (EPCAM) also called 17-1A antigen
 XX
 SO Sequence 1630 BP; 376 A; 484 C; 437 G; 333 T; 0 U; 0 Other;

Query Match 79.6%; Score 255.4; DB 3; Length 1630;
 Best Local Similarity 87.2%; Pred. No. 56-73;
 Matches 280; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCCATCCCTGCTGCTTCTGTGGAGACAGATCAC 60
 DB 96 GAGCTCCAGATGACCCAGTCCATCCCTGCTGCTGCTGTGAGAGACAGATCAC 155
 QY 61 ATCACTTGTGAGACAAGTCAGAGCATTTAGACGCTATTAAATTGGTATCAGCAAAACA 120
 DB 156 ATCACTTGTGCGGCAAGTCAGAGCATTTAGACGCTATTAAATTGGTATCAGCAAAACA 215
 QY 121 GACAGCCTCTTAAGCTGCTATTATGCGGATTCACCCGGGAATCCGGGCTCCTGAC 180
 DB 216 GACAGCCTCTTAAGCTGCTATTATGCGGATTCACCCGGGAATCCGGGCTCCTGAC 275
 QY 181 CGATTTCAGTGGACGCGGCTGCGGACAGATTTCACCTCACCATCAGAGCTCAACCT 240
 DB 276 CGATTTCAGTGGACGCGGCTGCGGACAGATTTCACCTCACCATCAGAGCTCAACCT 335
 QY 241 GAAGATTCCTGCACTTACTACTCTGACAGAGTATGACATCCGCTACCTTTGGCCAG 300
 DB 336 GAAGATTTTGTCTACTTACTTTTGTCAACAGCTGACAGTTTGGCATCCTTCGACCA 395
 QY 301 GGGACCAAGCTGGAGATCAAA 321
 DB 396 GGGACAGACTGCAGATTCAA 416

RESULT 6
 AAT66781
 ID AAT66781 standard; cDNA, 321 BP.
 AC AAT66781;
 XX
 DT 29-JAN-1998 (first entry)
 XX
 DE Anti-cancer specific antigen MAb light chain variable region cDNA.
 XX
 KM Light chain; variable region; cancer specific antigen; human;
 KM monoclonal antibody; hMab; diagnosis; cancer; immunotherapy;
 KM purification; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT mat_peptide 1..321
 FT /*tag= a
 XX
 PN JP09098786-A.
 XX
 PD 15-APR-1997.
 XX
 PF 06-OCT-1995; 95JP-00284400.
 XX
 PR 06-OCT-1995; 95JP-00284400.
 XX
 PA (MOMI) MORINAGA & CO LTD.
 PA (SHKJ) SHINGIYUTSU JIGYODAN.
 XX

DR MPI; 1997-275445/25.
 DR P-PSDB; AAM16649.
 XX CDNA encoding human monoclonal antibody - useful in medicine, or to
 PT purify cancer specific antigen.
 XX
 PS Claim 2; Fig 2; 7pp; Japanese.
 XX
 CC The present sequence encodes the light chain variable region of an anti-
 CC cancer specific antigen human monoclonal antibody (hMab). The hMab can be
 CC used in medicine, e.g. clinical diagnosis of cancer or immunotherapy, or
 CC to purify cancer specific antigen. The industrial scale production of
 CC large amounts of the hMab is made feasible by genetic engineering using
 CC the hMab cDNA
 XX
 SQ Sequence 321 BP; 86 A; 89 C; 72 G; 74 T; 0 U; 0 Other;
 Query Match 76.6%; Score 245.8; DB 2; Length 321;
 Best Local Similarity 85.4%; Pred. No. 3.6e-70;
 Matches 274; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
 QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTCTGCTGGAGACAGAGTCACC 60
 DB 1 GACATCCAGATGACCCAGTCTCCATCTCCCTGCTCTGCTGGAGACAGAGTCACC 60
 QY 61 ATCACTTTCGCAAGTCAAGCATTTAGACAGCTTAAATTTGGTATCAGCAAAACCA 120
 DB 61 ATCACTTTCGCGGCAAGTCAAGCATTTAGACAGCTTAAATTTGGTATCAGCAAAACCA 120
 QY 121 GGACAGCTCTTAAGTGTCTATTCTGCGCATCTACCGGGAATCCGGGGTCCCTGAC 180
 DB 121 GGGAAGCCCCCTTAAGTGTCTATTCTGCGCATCTACCGGGAATCCGGGGTCCCTATCA 180
 QY 181 CGATTGAGTGGACGCGGCTCTGGAGACAGATTCTCACTCAATCAGATCTACAACT 240
 DB 181 AGGTTGAGTGGACGCGGATCTGGAGACAGATTCTCACTCAATCAGATCTGCAACT 240
 QY 241 GAAGATTTCGCAACTTACTACTGTCAAGAGATTAGACATCCCGTACACTTTGGCCAG 300
 DB 241 GAAGATTTCGCAACTTACTACTGTCAAGAGATTAGACATCCCGTACACTTTGGCCAG 300
 QY 301 GGGACCAAGCTGAGATCAAA 321
 DB 301 GGGACCAAGCTGAGATCAAA 321
 RESULT 7
 AAH74685
 ID AAH74685 standard; DNA; 333 BP.
 XX
 AC AAH74685;
 XX
 DT 29-OCT-2001 (first entry)
 XX
 DE Nucleotide sequence of the L chain variable region of ScFv3-4.
 XX
 KW Complementarity determining region; CDR; single chain antibody; ScFv;
 KW hepatitis C virus; HCV; HCV infection; CD81; E2 protein; NS1 protein;
 KW envelope glycoprotein; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200158459-A1.
 XX
 PD 16-AUG-2001.
 XX
 PF 13-FEB-2001; 2001WO-JP000967.
 XX
 PR 14-FEB-2000; 2000JP-00034906.
 XX
 PA (MITS-) MITSUBISHI-TOKYO PHARM INC.
 XX
 PI Itami S, Shibui T, Seki M, Yotsumoto Y, Matsuura Y, Miyamura T;

XX MPI; 2001-496986/54.
 DR P-PSDB; AAG63656.
 XX
 PT Remedies for hepatitis C containing substances with antiviral effects
 PT e.g. antibodies, proteins, sulfated polysaccharides and low-molecular
 PT compounds, by inhibiting binding of hepatitis C virus envelope
 glycoprotein or CD81.
 XX
 PS Claim 40; Page 119-120; 138pp; Japanese.
 XX
 CC The present sequence encodes the L chain variable region of a single
 CC chain antibody of the invention. The specification describes a substance
 CC can inhibit the binding between hepatitis C virus (HCV) and cells with
 CC potential HCV infection, cells with expression of CD81, or CD81. This
 CC substance is especially an antibody with affinity towards HCV E2/NS1
 CC protein, containing amino acid sequences based on the complementarity
 CC determining region (CDR) 1, CDR2 and CDR3 of the H and L chain variable
 CC regions. The antibody inhibits the viral envelope glycoprotein. It is
 CC also a CD81 inhibitor. The antibodies and drugs are used for treatment
 CC and/or prevention of hepatitis C, or for diagnosis of hepatitis C
 XX
 SQ Sequence 333 BP; 87 A; 89 C; 77 G; 80 T; 0 U; 0 Other;
 Query Match 75.6%; Score 242.6; DB 5; Length 333;
 Best Local Similarity 84.7%; Pred. No. 4.1e-69;
 Matches 272; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
 QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTCTGCTGGAGACAGAGTCACC 60
 DB 1 GACATGATATGACCCAGTCTCCATCTCCCTGCTCTGCTGGAGACAGAGTCACC 60
 QY 61 ATCACTTTCGCAAGTCAAGCATTTAGACAGCTTAAATTTGGTATCAGCAAAACCA 120
 DB 61 ATCACTTTCGCGGCAAGTCAAGCATTTAGACAGCTTAAATTTGGTATCAGCAAAACCA 120
 QY 121 GGACAGCTCTTAAGTGTCTATTCTGCGCATCTACCGGGAATCCGGGGTCCCTGAC 180
 DB 121 GGGAAGCCCCCTTAAGTGTCTATTCTGCGCATCTACCGGGAATCCGGGGTCCCTATCA 180
 QY 181 CGATTGAGTGGACGCGGCTCTGGAGACAGATTCTCACTCAATCAGATCTACAACT 240
 DB 181 AGGTTGAGTGGACGCGGATCTGGAGACAGATTCTCACTCAATCAGATCTGCAACT 240
 QY 241 GAAGATTTCGCAACTTACTACTGTCAAGAGATTAGACATCCCGTACACTTTGGCCAG 300
 DB 241 GAAGATTTCGCAACTTACTACTGTCAAGAGATTAGACATCCCGTACACTTTGGCCAG 300
 QY 301 GGGACCAAGCTGAGATCAAA 321
 DB 301 GGGACCAAGCTGAGATCAAA 321
 RESULT 8
 ABT34321
 ID ABT34321 standard; DNA; 333 BP.
 XX
 AC ABT34321;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Hepatitis C virus treatment related human DNA sequence SEQ ID No 33.
 XX
 KW Virucide; inhibit; binding; hepatitis C virus; HCV; E2/NS1 protein;
 KW antibody; recombinant; antiviral; infection; human; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2003014728-A1.
 XX
 PD 20-FEB-2003.
 XX
 PF 09-AUG-2002; 2002WO-JP008175.

XX 10-AUG-2001; 2001JP-00243947.
XX (MITS-) MITSUBISHI PHARMA CORP.
XX (NINA-) JAPAN AGENCY NAT INST HEALTH.
XX Itami S, Seki M, Kito M, Matsuura Y, Miyamura T;
XX WPI; 2003-248334/24.
XX
XX Pharmaceutical compositions for hepatitis C containing screened
XX inhibitors of binding between hepatitis virus (HCV) E2/NS1 protein and
XX antibody, useful in preventing or treating HCV infections.
XX
XX Example 4; Page 88; 136pp; Japanese.
XX
XX The invention relates to a novel method for screening substances
XX inhibiting the binding of hepatitis C virus (HCV) E2/NS1 protein to an
XX antibody having an affinity for the protein. The novel method comprises:
XX contacting the protein with any of the antibodies selected, from those
XX described in the specification, in the presence or absence of a test
XX substance; and comparing the binding results. Compositions comprising the
XX (recombinant) antibodies are useful as antivirals and are especially
XX useful in preventing or treating HCV (hepatitis C) infections. This
XX polynucleotide sequence represents a human DNA sequence relating to the
XX novel HCV therapy method of the invention
XX
XX Sequence 333 BP; 87 A; 89 C; 77 G; 80 T; 0 U; 0 Other;
XX
XX Query Match 75.6%; Score 242.6; DB 10; Length 333;
XX Best Local Similarity 84.7%; Pred. No. 4.1e-69;
XX Matches 272; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
XX
QY 1 GAGCTCCAGATGAGCCAGTCTCCCTCTGCTTGTGTGGAGACAGAGTACC 60
DB 1 GACATCGTATGAGCCAGTCTCCCTCTGCTGATCTGTAGAGAGACAGAGTACC 60
QY 61 ATACTTGTGCGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 120
DB 61 ATACTTGTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
QY 121 GGAAGAGCTTCTAAGCTGTCTATTTAAGTGTGACGACGACGACGACGACGAC 180
DB 121 GGAAGAGCTTCTAAGCTGTCTATTTAAGTGTGACGACGACGACGACGACGAC 180
QY 181 CGATTGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
DB 181 AGGTTGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
QY 241 GAAAGATTCTGCACTTACTGTCAGAGATTAGAGACGACGACGACGACGACGAC 300
DB 241 GAAAGATTCTGCACTTACTGTCAGAGATTAGAGACGACGACGACGACGACGAC 300
QY 301 GGGACCAAGCTGAGATCAAA 321
DB 301 GGGACCAAGCTGAGATCAAA 321
XX
XX RESULT 9
XX ABT34316
XX ID ABT34316 standard; DNA; 720 BP.
XX
XX ABT34316;
XX
XX 12-JUN-2003 (first entry)
XX Hepatitis C virus treatment related human DNA sequence SEQ ID No 8.
XX
XX Vmucide; inhibit; binding; hepatitis C virus; HCV; E2/NS1 protein;
XX antibody; recombinant; antiviral; infection; human; gene; ds.
XX
XX Homo sapiens.
XX

PN W02003014728-A1.
XX 20-FEB-2003.
XX
XX 09-AUG-2002; 2002WO-JP008175.
XX
XX 10-AUG-2001; 2001JP-00243947.
XX
XX (MITS-) MITSUBISHI PHARMA CORP.
XX (NINA-) JAPAN AGENCY NAT INST HEALTH.
XX Itami S, Seki M, Kito M, Matsuura Y, Miyamura T;
XX WPI; 2003-248334/24.
XX
XX Pharmaceutical compositions for hepatitis C containing screened
XX inhibitors of binding between hepatitis virus (HCV) E2/NS1 protein and
XX antibody, useful in preventing or treating HCV infections.
XX
XX Claim 11; Page 71-73; 136pp; Japanese.
XX
XX The invention relates to a novel method for screening substances
XX inhibiting the binding of hepatitis C virus (HCV) E2/NS1 protein to an
XX antibody having an affinity for the protein. The novel method comprises:
XX contacting the protein with any of the antibodies selected, from those
XX described in the specification, in the presence or absence of a test
XX substance; and comparing the binding results. Compositions comprising the
XX (recombinant) antibodies are useful as antivirals and are especially
XX useful in preventing or treating HCV (hepatitis C) infections. This
XX polynucleotide sequence represents a human DNA sequence relating to the
XX novel HCV therapy method of the invention
XX
XX Sequence 720 BP; 188 A; 196 C; 175 G; 161 T; 0 U; 0 Other;
XX
XX Query Match 75.6%; Score 242.6; DB 10; Length 720;
XX Best Local Similarity 84.7%; Pred. No. 5.7e-69;
XX Matches 272; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
XX
QY 1 GAGCTCCAGATGAGCCAGTCTCCCTCTGCTTGTGTGGAGACAGAGTACC 60
DB 61 GACATCGTATGAGCCAGTCTCCCTCTGCTGATCTGTAGAGAGACAGAGTACC 120
QY 61 ATACTTGTGCGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 120
DB 61 ATACTTGTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
QY 121 GGAAGAGCTTCTAAGCTGTCTATTTAAGTGTGACGACGACGACGACGACGAC 180
DB 121 GGAAGAGCTTCTAAGCTGTCTATTTAAGTGTGACGACGACGACGACGACGAC 180
QY 181 CGATTGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
DB 181 AGGTTGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
QY 241 GAAAGATTCTGCACTTACTGTCAGAGATTAGAGACGACGACGACGACGACGAC 300
DB 241 GAAAGATTCTGCACTTACTGTCAGAGATTAGAGACGACGACGACGACGACGAC 300
QY 301 GGGACCAAGCTGAGATCAAA 321
DB 361 GGGACCAAGCTGAGATCAAA 381
XX
XX RESULT 10
XX AAH74689
XX ID AAH74689 standard; DNA; 900 BP.
XX
XX AAH74689;
XX
XX 29-OCT-2001 (first entry)
XX Nucleotide sequence of single chain antibody ScFv3-4.
XX
XX

KM Complementarity determining region; CDR: single chain antibody; ScFv;
 KM hepatitis C virus; HCV; HCV infection; CD81; E2 protein; NS1 protein;
 KM envelope glycoprotein; ss.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 1..900
 FT /-tag= a
 FT /product= "ScFv 3-4"
 XX
 XX MO200158459-A1.
 XX
 XX 16-AUG-2001.
 XX
 XX 13-FEB-2001; 2001WO-JP000967.
 XX
 XX 14-FEB-2000; 2000JP-00034906.
 XX
 XX (MITS-) MITSUBISHI-TOKYO PHARM INC.
 XX
 XX Itami S, Shibui T, Seki M, Yotsumoto Y, Matsuura Y, Miyamura T;
 PI
 DR WPI; 2001-496986/54.
 DR P-PSDB; AAG63660.
 XX
 XX Remedies for hepatitis C containing substances with antiviral effects
 PT e.g. antibodies, proteins, sulfated polysaccharides and low-molecular
 PT compounds, by inhibiting binding of hepatitis C virus envelope
 PT glycoprotein or CD81.
 XX
 XX
 XX Claim 38; Page 127-129; 138pp; Japanese.
 XX
 CC The present sequence encodes a single chain antibody of the invention.
 CC The specification describes a substance can inhibit the binding between
 CC hepatitis C virus (HCV) and cells with potential HCV infection, cells
 CC with expression of CD81, or CD81. This substance is especially an
 CC antibody with affinity towards HCV E2/NS1 protein, containing amino acid
 CC sequences based on the complementarity determining region (CDR) 1, CDR2
 CC and CDR3 of the H and L chain variable regions. The antibody inhibits the
 CC viral envelope glycoprotein. It is also a CD81 inhibitor. The antibodies
 CC and drugs are used for treatment and/or prevention of hepatitis C, or for
 CC diagnosis of hepatitis C
 CC
 SQ Sequence 900 BP; 198 A; 244 C; 259 G; 199 T; 0 U; 0 Other;
 Query Match 75.6%; Score 242.6; DB 5; Length 900;
 Best Local Similarity 84.7%; Pred. No. 6.3e-69;
 Matches 272; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
 QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCTGCTGCTTCTGTGGAGACAGAGTCACC 60
 DB 496 GACATCGTATGACCCAGTCTCCATCTCTGCTGCTGATCTAGAGACAGAGTCACC 555
 QY 61 ATACTCTTGCGGACAGTACAGACATTAAGAGCTATTAATGATACGAGAAACCA 120
 DB 556 ATACTCTTGCGGACAGTACAGACATTAAGAGCTATTAATGATACGAGAAACCA 615
 QY 121 GGCAGACCTCTTAAGCTGCTCATTTTACTGGCGATCTACCGGGAATCCGGGTCCTGAC 180
 DB 616 GGGAAAGCCCCCTAAGCTCTGCTGCTATGCTGATCTAATTTGGCAAAGTGGGTCCTATCA 675
 QY 181 CGATTCACTGCGAGCGGGTCTGGAGACAGATTTCACTCTCAATCAGACAGTCTCAACCT 240
 DB 676 AGGTTCACTGCGAGCGGGTCTGGAGACAGATTTCACTCTCAATCAGACAGTCTCAACCT 735
 QY 241 GAGGATTTGCGAGCGGGTCTGGAGACAGATTTCACTCTCAATCAGACAGTCTCAACCT 300
 DB 736 GAGGATTTGCGAGCGGGTCTGGAGACAGATTTCACTCTCAATCAGACAGTCTCAACCT 795
 QY 301 GGGACCAAGCTGAGATCAAA 321
 DB 796 GGGACCAAGCTGAGATCAAA 816

RESULT 11
 ID ABT34325
 XX ABT34325 standard; DNA; 900 BP.
 XX
 AC ABT34325;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Hepatitis C virus treatment related human DNA sequence SEQ ID No 37.
 XX
 XX Virucide; inhibit; binding; hepatitis C virus; HCV; E2/NS1 protein;
 KM antibody; recombinant; antiviral; infection; human; gene; ds.
 XX
 OS Homo sapiens.
 XX
 XX MO2003014728-A1.
 XX
 XX 20-FEB-2003.
 XX
 XX 09-AUG-2002; 2002WO-JP008175.
 XX
 XX 10-AUG-2001; 2001JP-00243947.
 XX
 XX (MITS-) MITSUBISHI PHARMA CORP.
 XX (NINA-) JAPAN AGENCY NAT INST HEALTH.
 XX
 XX Itami S, Seki M, Kito M, Matsuura Y, Miyamura T;
 PI
 DR WPI; 2003-248334/24.
 XX
 PT Pharmaceutical compositions for hepatitis C containing screened
 PT inhibitors of binding between hepatitis virus (HCV) E2/NS1 protein and
 PT antibody, useful in preventing or treating HCV infections.
 XX
 XX
 PS Claim 1; Page 96-98; 136pp; Japanese.
 XX
 CC The invention relates to a novel method for screening substances
 CC inhibiting the binding of hepatitis C virus (HCV) E2/NS1 protein to an
 CC antibody having an affinity for the protein. The novel method comprises:
 CC contacting the protein with any of the antibodies selected, from those
 CC described in the specification, in the presence or absence of a test
 CC substance; and comparing the binding results. Compositions comprising the
 CC (recombinant) antibodies are useful as antivirals and are especially
 CC useful in preventing or treating HCV (hepatitis C) infections. This
 CC polynucleotide sequence represents a human DNA sequence relating to the
 CC novel HCV therapy method of the invention
 CC
 SQ Sequence 900 BP; 198 A; 244 C; 259 G; 199 T; 0 U; 0 Other;
 Query Match 75.6%; Score 242.6; DB 10; Length 900;
 Best Local Similarity 84.7%; Pred. No. 6.3e-69;
 Matches 272; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
 QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCTGCTGCTTCTGTGGAGACAGAGTCACC 60
 DB 496 GACATCGTATGACCCAGTCTCCATCTCTGCTGCTGATCTAGAGACAGAGTCACC 555
 QY 61 ATACTCTTGCGGACAGTACAGACATTAAGAGCTATTAATGATACGAGAAACCA 120
 DB 556 ATACTCTTGCGGACAGTACAGACATTAAGAGCTATTAATGATACGAGAAACCA 615
 QY 121 GGCAGACCTCTTAAGCTGCTCATTTTACTGGCGATCTACCGGGAATCCGGGTCCTGAC 180
 DB 616 GGGAAAGCCCCCTAAGCTCTGCTGCTATGCTGATCTAATTTGGCAAAGTGGGTCCTATCA 675
 QY 181 CGATTCACTGCGAGCGGGTCTGGAGACAGATTTCACTCTCAATCAGACAGTCTCAACCT 240
 DB 676 AGGTTCACTGCGAGCGGGTCTGGAGACAGATTTCACTCTCAATCAGACAGTCTCAACCT 735
 QY 241 GAGGATTTGCGAGCGGGTCTGGAGACAGATTTCACTCTCAATCAGACAGTCTCAACCT 300

Db 736 GAAGATTTTGGAACTTACTACTGTCAACAGAGTTACACTATTCGGTACACTTTGGCCAG 795
 QY 301 GGGACCAAGCTGGAGATCAAA 321
 Db 796 GGGACCAAGCTGGAGATCAAA 816

RESULT 12

AAH68701
 ID AAH68701 standard; DNA; 321 BP.

XX AAH68701;

DT 14-SEP-2001 (first entry)

DE Human anti-Rh(D) antibody clone SH13 nucleotide sequence.

KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;

KW red blood cell; Rh phenotype; diagnosis; therapeutic; ds.

XX Homo sapiens.

XX US6255455-B1.

PD 03-JUL-2001.

PF 29-JAN-1999; 99US-00240274.

PR 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.

PR 10-APR-1998; 98US-0081380P.

PA (UYPE-) UNIV PENNSYLVANIA.

PI Siegel DL;

DR WPI; 2001-388931/41.

DR P-PSDB; AAG93644.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

The present invention describes an isolated Rh(D) binding protein, preferably a human antibody, (I) having an amino acid sequence comprising one of the sequences (S) given in AAG93558 to AAG93669. (I) has immunostimulant activity, and can be used as an immune system stimulant. (I) can be used in diagnostic and therapeutic medicine. The antibodies are used in diagnostics that require human antibodies instead of animal antibodies, such as determine the Rh phenotype of human red blood cells. AAH68615 to AAH68726 represent the nucleotide sequence which encode AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy chain CDR3 amino acid sequences which are given in the exemplification of the present invention.

Sequence 321 BP; 84 A; 89 C; 74 G; 74 T; 0 U; 0 Other;

Query Match 74.5%; Score 239.2; DB 5; Length 321;
 Best Local Similarity 84.8%; Pred. No. 5.3e-68;
 Matches 268; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 6 CCAGATGACCCAGCTCCATCCCTGCTGCTGCTGAGAGACAGAGTACCATCAG 65
 Db 3 CGAGCTACCCAGCTCCATCCCTGCTGCTGCTGAGAGACAGAGTACCATCAG 62
 QY 66 TTGTGGAACAGTCAAGAGCATTAGAGCTATTAAATTGGTATCAGAGAAACAGAGCA 125
 Db 63 TTGCGGAGCAAGTCAAGAGCATTAGAGCTATTAAATTGGTATCAGAGAAACAGAGCA 122
 QY 126 GCGTCTAAGCTGCTCATTACTGCGGATGATCCCGGAAATCCGGGATCCCTGACCATTT 185

Db 123 AGCCCCTAAGCTCCGATCTTANGTCGATCCAGTTTGGCAAGTGGGATCCATCAAGGTT 182
 QY 186 CAGTGGCAGCGGATCTGGAGACAGATTTCATCTCAACATCAGAGTCAAACTGGAAGA 245
 Db 183 CAGTGGCAGTGAATCTGGAGACAGATTTCATCTCAACATCAGAGTCAAACTGGAAGA 242
 QY 246 TTGTGCAACTTACTACTGTGACAGAGTTAGACATCCCGTACACTTTTGGCCAGGGGAC 305
 Db 243 TTTTGCACCTTACTACTGTGACAGAGTTAGACATCCCGTACACTTTTGGCCAGGGGAC 302
 QY 306 CAAGCTGAGATCAAA 321
 Db 303 CAAGCTGAGATCAAA 318

RESULT 13

ACD45365
 ID ACD45365 standard; DNA; 321 BP.

XX ACD45365;

DT 12-SEP-2003 (first entry)

DE Anti-Rh(D) light chain SH13 DNA.

KW Human; ds; gene; RH(D) binding protein; blood typing; blood product;

KW magnetically activated cell sorting.

XX Homo sapiens.

PN US2003040605-A1.

PD 27-FEB-2003.

PF 04-MAY-2001; 2001US-00848798.

PR 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.

PR 10-APR-1998; 98US-0081380P.

PR 29-JAN-1999; 99US-00240274.

PA (UYPE-) UNIV PENNSYLVANIA.

PI Siegel DL;

DR WPI; 2003-512273/48.

DR P-PSDB; ABO27451.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

New human Rh(D)-binding protein useful for various diagnostic and therapeutic applications, including typing of blood or blood products.
 Claim 12; Page 57; 187pp; English.

The invention relates to an isolated Rh(D) binding protein. The protein can be used for magnetically activated cell sorting. The protein is useful in various diagnostic and therapeutic applications in humans, including typing of blood or blood products. The present sequence represents DNA encoding a human anti-Rh(D) chain

Query Match 74.5%; Score 239.2; DB 9; Length 321;
 Best Local Similarity 84.8%; Pred. No. 5.3e-68;
 Matches 268; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 6 CCAGATGACCCAGCTCCATCCCTGCTGCTGCTGAGAGACAGAGTACCATCAG 65
 Db 3 CGAGCTACCCAGCTCCATCCCTGCTGCTGCTGAGAGACAGAGTACCATCAG 62
 QY 66 TTGTGGAACAGTCAAGAGCATTAGAGCTATTAAATTGGTATCAGAGAAACAGAGCA 125
 Db 63 TTGCGGAGCAAGTCAAGAGCATTAGAGCTATTAAATTGGTATCAGAGAAACAGAGCA 122

OY		126	GGCTCCTAAGCGTCAATTTACGAGGATCCCGGGAATCCGGGGGTCCCTACCGATT	185
Dd		123	AGCCCCTAGCTTCCTGATCTTAAGCTCATCCATTTTGCAAGTGGGGTCCCATCAAGGTT	182
OY		186	CAGTGGCAGCGGGGTCTGGACAGATTTCACTCTCACCATCAGCAGTCTACAACTTGAGA	245
Dd		183	CAGTGGCAGTGGATCTGGGACAGATTTTCACTCTCACCATCAGCAGTCTGCAACTGAAGA	242
OY		246	TTTCTGCAACTTACTACTGTGCAGACAGTTTACGACATCCGTTACACTTTTGGCCAGGGGAC	305
Dd		243	TTTTGCCAACTTACTACTGTGCACAGAGTTACAGTACCCTCTACACTTTTGGCCAGGGGAC	302
OY		306	CAAGCTGGAGATCAAA 321	
Dd		303	CAAGCTGGAGATCAAAA 318	
 RESULT 14 AAH74684				
ID	AAH74684	standard; DNA; 333 BP.		
XX AC	AAH74684;			
XX DT	29-OCT-2001	(first entry)		
XX XX	Nucleotide sequence of the L chain variable region of ScFv3-3.			
XX KW	Complementarity determining region; CDR; single chain antibody; ScFv;			
KW KW	hepatitis C virus; HCV; HCV infection; CD81; E2 protein; NS1 protein;			
KW KW	envelope glycoprotein; ss.			
OS OS	Homo sapiens.			
XX PN	WO2001S8459-A1.			
PD PD	16-AUG-2001.			
XX PF	13-FEB-2001; 2001WO-JP000967.			
XX PR	14-FEB-2000; 2000JP-00034906.			
PA PA	(MITS-) MITSUBISHI-TOKYO PHARM INC.			
P1 P1	Itami S, Shibui T, Seki M, Yotsumoto Y, Matsura Y, Miyamura T;			
DR DR	WPI; 2001-496986/54.			
PT PT	P-PsDB; AAG63655.			
PT PT	Remedies for hepatitis C containing substances with antiviral effects			
PT PT	e.g. antibodies, proteins, sulfated polysaccharides and low-molecular			
PT PT	glycoprotein or CD81.			
XX XX	Claim 40; Page 118-119; 138pp; Japanese.			
XX CC	The present sequence encodes the L chain variable region of a single			
CC CC	chain antibody of the invention. The specification describes a substance			
CC CC	can inhibit the binding between hepatitis C virus (HCV) and cells with			
CC CC	potential HCV infection, cells with expression of CD81, or CD81. This			
CC CC	substance is especially an antibody with affinity towards HCV E2/NS1			
CC CC	protein, containing amino acid sequences based on the complementarity			
CC CC	determining region (CDR) 1, CDR2 and CDR3 of the H and L chain variable			
CC CC	regions. The antibody inhibits the viral envelope glycoprotein. It is			
CC CC	also a CD81 inhibitor. The antibodies and drugs are used for treatment			
CC CC	and/or prevention of hepatitis C, or for diagnosis of hepatitis C			
SQ SQ	Sequence 333 BP; 87 A; 91 C; 80 G; 75 T; 0 U; 0 Other;			
 Query Match 74.1%; Score 237.8; DB 5; Length 333; Best Local Similarity 83.8%; Pred. No. 1.6e-67; Matches 269; Conservative 0; Mismatches 52; Indels 0; Gaps 0				
OY	1 GAGCTTCAGATGACCCAGTCTCCATCTCCCTGCTGCTTCTGTGGAGACAAGTCAACC 60			

Db	1	GACATCCAGATGACCCAGCTCCATCCCTCCTGCTGATCTGTAGAGACAGAGTACC	60
Qy	61	ATCACTTGTGGACAACTGACAGCAATTGACAGCTATTAAATTGGTATCAGCAGAAACCA	120
Db	61	ATCACTTGGCCGGGCAAGTCAGAGCACTTATGACAGCTATTAAATTGGTATCAGCAGAAACCA	120
Qy	121	GGACACCCCTCAAGTGTGCTCAATTACCTGCGGAGTCCACCCGGGAATCCGGGGTCCCTGAC	180
Db	121	GGGAAGCCCCCTTAAAGTCTCTGTATCTATGCTGCATCCAGTTTGCAGAAAGTGGGTCACATCA	180
Qy	181	CGAATCAGTGGGACGCGGCTGTGGGACAGATTTCATCTCAACATCAGCAGAGTCTAACACT	240
Db	181	AGGTTCAAGTGGGAGTGGAGTCTGGGACAGATTTCACTCTCAACATCAGAGAGTCTGCAACT	240
Qy	241	GAGGATTTCTGCAACTTACTACTGTGACGAGAGTTACGACATCCCGTACACTTTTGGCCAG	300
Db	241	GAGGATTTTGGCAACTTACTACTGTGACGAGAGTTACGATACCCGCTCACTTTCGGCGGA	300
Qy	301	GGGACCAAGCTGGAGATCAAA 321	
Db	301	GGGACCAAGGTGGAGATCAAA 321	
RESULT 15			
ABT34320	ID	ABT34320 standard; DNA; 333 BP.	
AC	ABT34320;		
XX	12-JUN-2003	(first entry)	
DE	Hepatitis C virus treatment related human DNA sequence SEQ ID No 32.		
XX	Virucide; inhibit; binding; hepatitis C virus; HCV; E2/NS1 protein;		
XX	antibody; recombinant; antiviral; infection; human; gene; ds.		
OS	Homo sapiens.		
XX	MO2003014728-A1.		
PN	20-FEB-2003.		
PD	09-AUG-2002; 2002MO-JP008175.		
PF	10-AUG-2001; 2001JP-00243947.		
XX	(MITS-) MITSUBISHI PHARMA CORP.		
XX	(NINA-) JAPAN AGENCY NAT INST HEALTH.		
XX	Item1 S, Seki M, Kito M, Matsura Y, Miyamura T;		
PI	WPI; 2003-248334/24.		
DR	Pharmaceutical compositions for hepatitis C containing screened		
PT	inhibitors of binding between hepatitis virus (HCV) E2/NS1 protein and		
PT	antibody, useful in preventing or treating HCV infections.		
XX	Example 4; Page 87; 136pp; Japanese.		
XX	The invention relates to a novel method for screening substances		
CC	inhibiting the binding of hepatitis C virus (HCV) E2/NS1 protein to an		
CC	antibody having an affinity for the protein. The novel method comprises:		
CC	contacting the protein with any of the antibodies selected, from those		
CC	described in the specification, in the presence or absence of a test		
CC	substance; and comparing the binding results. Compositions comprising the		
CC	(recombinant) antibodies are useful as antivirals and are especially		
CC	useful in preventing or treating HCV (hepatitis C) infections. This		
CC	polynucleotide sequence represents a human DNA sequence relating to the		
CC	novel HCV therapy method of the invention		
XX	Sequence 333 BP; 87 A; 91 C; 80 G; 75 T; 0 U; 0 Other;		

Query Match 74.1%; Score 237.8; DB 10; Length 333;
Best Local Similarity 83.8%; Pred. No. 1.6e-67;
Matches 269; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY	1	GAGCTCGAGTGA	CCGAGTCTCCATCCTCCTGTCTGTCTGTGTGGAGACAGAGTCACC	60
Db	1	GACATCCAGATGACC	CCAGTCTCCATCCTCCTGTCTGTGTGGAGACAGAGTCACC	60
QY	61	ATGACTTTCGGA	CAGATCAGAGCATTAGCAGCTATTAAATTGGTATCAGCAGAAACCA	120
Db	61	ATGACTTTCGGA	CAGATCAGAGCATTAGCAGCTATTAAATTGGTATCAGCAGAAACCA	120
QY	121	GGACAGCTCT	TAAGCTGCTCATTTACTGGCGATCTACCCGGGATCCGGGGTCCCTGAC	180
Db	121	GGGAAAGCCCT	TAAGCTGCTCATTTACTGGCGATCTACCCGGGATCCGGGGTCCCTGAC	180
QY	181	CGATTGAGTGG	CAGCGGGTCTGGGACAGATTTCACCTGACCATCAGCAGCTTACAACCT	240
Db	181	AGGTTGAGTGG	CAGCGGGTCTGGGACAGATTTCACCTGACCATCAGCAGCTTACAACCT	240
QY	241	GAAGATTTCGCA	ACTTACTGTGAGCAGAGTTTACGACATCCCGTACACTTTGGCCAG	300
Db	241	GAAGATTTCGCA	ACTTACTGTGAGCAGAGTTTACGACATCCCGTACACTTTGGCCAG	300
QY	301	GGGACCAAGCT	GGAGATCAA 321	
Db	301	GGGACCAAGCT	GGAGATCAA 321	

Search completed: December 7, 2004, 06:41:24
Job time : 274.757 secs

Db 303 CAAGCTGGAGATCAAA 318

RESULT 2

US-09-192-854-1

Sequence 1, Application US/09192854

Patent No. 6696245

GENERAL INFORMATION:

APPLICANT: Winter, Greg

APPLICANT: Tomlinson, Ian

TITLE OF INVENTION: Methods for Selecting Functional Peptides

FILE REFERENCE: 3789/72916

CURRENT APPLICATION NUMBER: US/09/192,854

EARLIER FILING DATE: 1998-11-17

EARLIER APPLICATION NUMBER: 60/066,729

NUMBER OF SEQ ID NOS: 212

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 720

TYPE: DNA

ORGANISM: Homo sapiens

US-09-192-854-1

Query Match 73.6%; Score 236.2; DB 4; Length 720;

Best Local Similarity 83.5%; Pred. No. 1e-70;

Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGATGCTCCATCTCTGCTGCTTGTGGAGACAGAGTCAAC 60

DB 397 GACATCCAGATGACCCAGATGCTCCATCTCTGCTGCTTGTGGAGACAGAGTCAAC 456

QY 61 ATGACTTTCGAGCAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 120

DB 457 ATGACTTTCGAGCAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 516

QY 121 GAGACAGCTCTGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180

DB 517 GGGAAAGCCCTGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 576

QY 181 CGATTCAGTGGAGCGGGTGTGGAGCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

DB 577 AGGTTCAGTGGAGCGGGTGTGGAGCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 636

QY 241 GAGATTCGCACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300

DB 637 GAGATTCGCACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 696

QY 301 GGGACCAAGCTGGAGTCAAA 321

DB 697 GGGACCAAGCTGGAGTCAAA 717

RESULT 3

US-09-240-274-113

Sequence 113, Application US/09240274

Patent No. 6255455

GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

FILE REFERENCE: 09596-4202

CURRENT APPLICATION NUMBER: US/09/240,274

EARLIER FILING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER FILING DATE: 1998-04-10

EARLIER APPLICATION NUMBER: 60/028,550

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 113

LENGTH: 321

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE: OTHER INFORMATION: anti-Rh(D) chain 113

US-09-240-274-113

Query Match 73.5%; Score 236; DB 3; Length 321;

Best Local Similarity 84.2%; Pred. No. 8.3e-71;

Matches 266; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 6 CCAGATGACCCAGATGCTCCATCTCTGCTGCTTGTGGAGACAGAGTCAACATCAAC 65

DB 3 CGAGCTACCCAGATGCTCCATCTCTGCTGCTTGTGGAGACAGAGTCAACATCAAC 62

QY 66 TTGTGGACAACTGACAGATTAAGACGATTAATAATTGGTATCGACGAACCGAGACA 125

DB 63 TTGTGGACAACTGACAGATTAAGACGATTAATAATTGGTATCGACGAACCGAGACA 122

QY 126 GCCTCTAAGTGTCTCATTTACTGAGCGATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185

DB 123 AGCCCTTAAGTGTCTCATTTACTGAGCGATCTACCCGGGAATCCGGGGTCCCTGACCGATT 182

QY 186 CAGTGGACAGCGGGTGTGGAGCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 245

DB 183 CAGTGGACAGCGGGTGTGGAGCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 242

QY 246 TTCTGCACTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 305

DB 243 TTCTGCACTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 302

QY 306 CAAGCTGGAGATCAAA 321

DB 303 CAAGCTGGAGATCAAA 318

RESULT 4

US-09-240-274-109

Sequence 109, Application US/09240274

Patent No. 6255455

GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

FILE REFERENCE: 09596-4202

CURRENT APPLICATION NUMBER: US/09/240,274

EARLIER FILING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER FILING DATE: 1998-04-10

EARLIER APPLICATION NUMBER: 60/028,550

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 109

LENGTH: 321

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE: OTHER INFORMATION: anti-Rh(D) chain 109

US-09-240-274-109

Query Match

Best Local Similarity 72.0%; Score 231.2; DB 3; Length 321;

Matches 263; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 6 CCAGATGACCCAGATGCTCCATCTCTGCTGCTTGTGGAGACAGAGTCAACATCAAC 65

DB 3 CGAGCTACCCAGATGCTCCATCTCTGCTGCTTGTGGAGACAGAGTCAACATCAAC 62

QY 66 TTGTGGACAACTGACAGATTAAGACGATTAATAATTGGTATCGACGAACCGAGACA 125

DB 63 TTGTGGACAACTGACAGATTAAGACGATTAATAATTGGTATCGACGAACCGAGACA 122

QY 126 GCCTCTAAGTGTCTCATTTACTGAGCGATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185

Db 183 CAGTGGACAGTCTGCGGACAGATTTCATCTCACCATCAGACAGTCTGCAACTGGAAGA 242
QY 246 TTGTGCACTTACTACTGTGTCAGAGAGTTTACGATCCGTCACATTTTGGCCAGGGGAC 305
Db 243 TTGTGCACTTACTACTGTGTCAGAGAGTTTACGATCCGTCACATTTTGGCCAGGGGAC 302
QY 306 CAGCTGGAGATCAAA 321
Db 303 CAGCTGGAGATCAAA 318

RESULT 13

US-09-240-274-108
; Sequence 108, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274

EARLIER FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
NUMBER OF SEQ ID NOS: 224

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 108

LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
OTHER INFORMATION: anti-Rh(D) chain 108

US-09-240-274-108

Query Match

70.5%; Score 226.4; DB 3; Length 321;
Best Local Similarity 82.3%; Pred. No. 1.6e-67;
Matches 260; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 6 CCAATGACCCAGTCTTCATCTCTCTGCTTGTGCGAGACAGAGTCAACATCAC 65
Db 3 CGAGTCAACCCAGTCTTCATCTCTCTGCTTGTGCGAGACAGAGTCAACATCAC 62
QY 66 TTGTGGAACAAGTCAGAGATTTAGAGCATTTAAATTTGGTACAGAGAAACAGAGAA 125
Db 63 TTGTGGAACAAGTCAGAGATTTAGAGCATTTAAATTTGGTACAGAGAAACAGAGAA 122
QY 126 GCCTCTTAAGCTGCTCATTTACTGCGAGATCTACCCGGAATCCGGGGTCCCTGACCGATT 185
Db 123 AGCCCTTAAGCTGCTCATTTACTGCGAGATCTACCCGGAATCCGGGGTCCCTGACCGATT 182
QY 186 CAGTGGACAGGGGTCTGGGACAGATTTCACTCTCACCATCAGAGATCTTCAACCTGAAGA 245
Db 183 CAGTGGACAGGGGTCTGGGACAGATTTCACTCTCACCATCAGAGATCTTCAACCTGAAGA 242
QY 246 TTGTGCACTTACTACTGTGTCAGAGAGTTTACGATCCGTCACATTTTGGCCAGGGGAC 305
Db 243 TTGTGCACTTACTACTGTGTCAGAGAGTTTACGATCCGTCACATTTTGGCCAGGGGAC 302
QY 306 CAGCTGGAGATCAAA 321
Db 303 CAGCTGGAGATCAAA 318

RESULT 14

US-09-240-274-201
; Sequence 201, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
EARLIER FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 201
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH20

FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 201
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH16

US-09-240-274-201

Query Match

70.5%; Score 226.4; DB 3; Length 321;
Best Local Similarity 82.3%; Pred. No. 1.6e-67;
Matches 260; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 6 CCAATGACCCAGTCTTCATCTCTCTGCTTGTGCGAGACAGAGTCAACATCAC 65
Db 3 CGAGTCAACCCAGTCTTCATCTCTCTGCTTGTGCGAGACAGAGTCAACATCAC 62
QY 66 TTGTGGAACAAGTCAGAGATTTAGAGCATTTAAATTTGGTACAGAGAAACAGAGAA 125
Db 63 TTGTGGAACAAGTCAGAGATTTAGAGCATTTAAATTTGGTACAGAGAAACAGAGAA 122
QY 126 GCCTCTTAAGCTGCTCATTTACTGCGAGATCTACCCGGAATCCGGGGTCCCTGACCGATT 185
Db 123 AGCCCTTAAGCTGCTCATTTACTGCGAGATCTACCCGGAATCCGGGGTCCCTGACCGATT 182
QY 186 CAGTGGACAGGGGTCTGGGACAGATTTCACTCTCACCATCAGAGATCTTCAACCTGAAGA 245
Db 183 CAGTGGACAGGGGTCTGGGACAGATTTCACTCTCACCATCAGAGATCTTCAACCTGAAGA 242
QY 246 TTGTGCACTTACTACTGTGTCAGAGAGTTTACGATCCGTCACATTTTGGCCAGGGGAC 305
Db 243 TTGTGCACTTACTACTGTGTCAGAGAGTTTACGATCCGTCACATTTTGGCCAGGGGAC 302
QY 306 CAGCTGGAGATCAAA 321
Db 303 CAGCTGGAGATCAAA 318

RESULT 15

US-09-240-274-203
; Sequence 203, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274

EARLIER FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380

EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550

NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 203
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH20

US-09-240-274-203

Query Match

70.5%; Score 226.4; DB 3; Length 321;
Best Local Similarity 82.3%; Pred. No. 1.6e-67;

US-09-240-274-203

	Matches	260;	Conservative	0;	Mismatches	56;	Indels	0;	Gaps	0;
Qy	6	CCAGATGACCCAGTCTTCATCTCTCCCTGCTGCTTCTGTGGGAGACAGAGTCAACCATCAC	65.							
Db	3	CGAGCTCACCCAGTCTTCATCTCTCCCTGCTGCTGCTGTGGGAGACAGAGTCAACCATTAAC	62							
Qy	66	TTGTGGAGACAGATGAGATTAAGAGTAAATTTGGTATCAGAGAAAACAGAGACA	125							
Db	63	TTGCCGGGCAAGTCAGAGCATTAAGCAGGTCCTTTAAATGGTATCAACATTAACCAAGGGGA	122							
Qy	126	GCCTCCTAAGCTGCTCATTTACTGTGGGATCTACCCGGGAATCCGGGGTCCCTGACCGATT	185							
Db	123	AGCCCTTAAGCTCTGATCTATGTGCAATCCAGCTGTGGGTCACACCGAGTT	182							
Qy	186	CAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACTGAAGA	245							
Db	183	CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA	242							
Qy	246	TTCTGCACTTCTACTGTGAGAGATTACGACATCCGATACCTTTGGCCAGGGGAC	305							
Db	243	CTTTGGACTTACTTCTGTACAGAGTGTGAGAAATCCGTACAGTTTGGCCAGGGGAC	302							
Qy	306	CAAGCTGAGATCAAA	321							
Db	303	CAAGCTGAGATCAAA	318							

Search completed: December 7, 2004, 08:57:54
Job time : 66.271 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 08:53:09 ; Search time 275.899 Seconds
(without alignments)
6393.344 Million cell updates/sec

Title: US-09-403-107-141

Perfect score: 321
Sequence: 1 gagctccagatgaccacgctc.....ggaccaagctgagatcaaa 321

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3695051 seqs, 2747533894 residues

Total number of hits satisfying chosen parameters: 7390102

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA.*
1: /cgn2_6/ptodata/2/pubpna/us07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PTCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	321	100.0	321	15	US-10-325-694-141 Sequence 141, App
2	255.4	79.6	321	15	US-10-325-694-147 Sequence 147, App
3	242.6	75.6	333	15	US-10-203-754A-61 Sequence 61, Appl
4	242.6	75.6	900	15	US-10-203-754A-65 Sequence 65, Appl
5	239.2	74.5	321	10	US-09-848-798-199 Sequence 199, Appl
6	237.8	74.1	333	15	US-10-203-754A-60 Sequence 60, Appl
7	237.8	74.1	900	15	US-10-203-754A-64 Sequence 64, Appl
8	236.2	73.6	324	17	US-10-344-514-3 Sequence 3, Appl
9	236.2	73.6	324	17	US-10-344-514-4 Sequence 4, Appl
10	236.2	73.6	720	9	US-09-192-854-1 Sequence 1, Appl
11	236.2	73.6	720	9	US-09-968-561A-1 Sequence 1, Appl
12	236.2	73.6	720	10	US-09-968-744A-1 Sequence 1, Appl

13	236.2	73.6	720	11	US-09-968-561A-1 Sequence 1, Appl
14	236.2	73.6	720	18	US-10-744-774-2 Sequence 2, Appl
15	236	73.5	321	10	US-09-848-798-113 Sequence 113, App
16	234.6	73.1	322	16	US-10-309-762-226 Sequence 119, App
17	234.6	73.1	322	16	US-10-309-762-227 Sequence 121, App
18	234.6	73.1	322	16	US-10-309-762-227 Sequence 227, App
19	234.6	73.1	322	16	US-10-308-591-54 Sequence 54, Appl
20	234.6	73.1	322	18	US-10-775-444A-54 Sequence 54, Appl
21	234.6	73.1	729	15	US-10-216-444-125 Sequence 125, App
22	233	72.6	322	16	US-10-384-933-125 Sequence 125, App
23	233	72.6	322	16	US-10-309-762-221 Sequence 221, App
24	231.4	72.1	321	17	US-10-663-244-78 Sequence 78, Appl
25	231.4	72.1	324	17	US-10-344-514-7 Sequence 7, Appl
26	231.4	72.1	324	17	US-10-344-514-8 Sequence 8, Appl
27	231.4	72.1	1106	16	US-10-264-049-121 Sequence 121, App
28	231.2	72.0	321	10	US-09-848-798-107 Sequence 107, App
29	229.8	71.6	324	18	US-10-409-814A-3 Sequence 109, App
30	229.8	71.6	384	16	US-10-309-762-115 Sequence 3, Appl
31	229.6	71.5	321	10	US-09-848-798-102 Sequence 115, App
32	229.6	71.5	321	10	US-09-848-798-218 Sequence 218, App
33	228.8	71.3	324	15	US-10-371-942-7 Sequence 7, Appl
34	228.8	71.3	324	15	US-10-371-942-19 Sequence 19, Appl
35	228.2	71.1	328	15	US-10-330-613-12 Sequence 12, Appl
36	228.2	71.1	328	15	US-10-330-530-12 Sequence 12, Appl
37	228.2	71.1	328	17	US-10-660-357-12 Sequence 12, Appl
38	228.2	71.1	387	9	US-09-905-243-27 Sequence 27, Appl
39	228	71.0	321	10	US-09-848-798-107 Sequence 107, App
40	227.8	71.0	324	10	US-09-848-798-101 Sequence 107, App
41	227.8	71.0	324	10	US-09-848-798-112 Sequence 112, App
42	227.8	71.0	324	10	US-09-848-798-210 Sequence 210, App
43	226.6	70.6	321	17	US-10-663-244-82 Sequence 82, Appl
44	226.6	70.6	714	14	US-10-153-382-18 Sequence 18, Appl
45	226.6	70.6	714	18	US-10-612-497-62 Sequence 62, Appl

ALIGNMENTS

RESULT 1				
US-10-325-694-141				
; Sequence 141, Application US/10325694				
; Publication No. US20030148463A1				
GENERAL INFORMATION:				
; APPLICANT: KUPER, PETER				
; APPLICANT: RAUM, TOBIAS				
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN				
; FILE REFERENCE: 38164000				
; CURRENT APPLICATION NUMBER: US/10/325,694				
; CURRENT FILING DATE: 2002-12-19				
; PRIOR APPLICATION NUMBER: US/09/403,107				
; PRIOR FILING DATE: 1999-10-14				
; NUMBER OF SEQ ID NOS: 152				
; SOFTWARE: PatentIn Ver. 2.1				
; SEQ ID NO 141				
; LENGTH: 321				
; TYPE: DNA				
; ORGANISM: HUMAN				
US-10-325-694-141				
Query Match				
Best Local Similarity 100.0%; Score 321; DB 15; Length 321;				
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	GAGCTCAGATGACCAAGCTCCTCCTGCTGCTTGTGTGGAGACAGATCACC	60	
DB	1	GAGCTCAGATGACCAAGCTCCTCCTGCTGCTTGTGTGGAGACAGATCACC	60	
QY	61	ATCACTTGTGGACAAGTACAGACATTAAGCTATTAATTTGATACAGAAACCA	120	
DB	61	ATCACTTGTGGACAAGTACAGACATTAAGCTATTAATTTGATACAGAAACCA	120	
QY	121	GAGACGCTCTTAAGTGTCTATTACTGTGGCATCAACCGGGAATCCGGGGTCCCTGAC	180	

```
Db      121 GGAACGCTCTTAAGTGGCTCATTTACTGGCGATCTACCGGGAATCCGGGGTCCCTGAC 180
Qy      181 CGATTAGTGGACGGGGTCTGGGACAGATTTCATCTCAATCAGACAGTCTCAACCT 240
Db      181 CGATTAGTGGACGGGGTCTGGGACAGATTTCATCTCAATCAGACAGTCTCAACCT 240
Qy      241 GAAGATTCTGCACTTACTACTGTGACAGAGTTAGACATCCCGTACCTTTGGCCAG 300
Db      241 GAAGATTCTGCACTTACTACTGTGACAGAGTTAGACATCCCGTACCTTTGGCCAG 300
Qy      301 GGGACCAAGCTGGAGATCAA 321
Db      301 GGGACCAAGCTGGAGATCAA 321
```

```
RESULT 2
US-10-325-694-147
; Sequence 147, Application US/10325694
; Publication No. US20030148463A1
; GENERAL INFORMATION:
; APPLICANT: KUPER, PETER
; APPLICANT: RAUM, TOBIAS
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
; FILE REFERENCE: 38164000
; CURRENT APPLICATION NUMBER: US/10/325,694
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/09/403,107
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 147
; LENGTH: 321
; TYPE: DNA
; ORGANISM: HUMAN
US-10-325-694-147
```

```
Query Match      79.6%; Score 255.4; DB 15; Length 321;
Best Local Similarity 87.2%; Pred. No. 1,4e-77;
Matches 280; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
```

```
Qy      1 GAGCTTCAGATGACCCAGTCTCCATCTCCCTGTGCTTGTGGAGACAGAGTCAAC 60
Db      1 GAGCTTCAGATGACCCAGTCTCCATCTCCCTGTGCTTGTGGAGACAGAGTCAAC 60
Qy      61 ATCACTTGTGGACAAAGTCAAGAGATTAAGCACTATTAATTTGGTATCAGAGAAACA 120
Db      61 ATCACTTGTGGACAAAGTCAAGAGATTAAGCACTATTAATTTGGTATCAGAGAAACA 120
Qy      121 GGAACGCTCTTAAGTGGCTCATTTACTGGCGATCTACCGGGAATCCGGGGTCCCTGAC 180
Db      121 GGAACGCTCTTAAGTGGCTCATTTACTGGCGATCTACCGGGAATCCGGGGTCCCTGAC 180
Qy      181 CGATTAGTGGACGGGGTCTGGGACAGATTTCATCTCAATCAGACAGTCTCAACCT 240
Db      181 CGATTAGTGGACGGGGTCTGGGACAGATTTCATCTCAATCAGACAGTCTCAACCT 240
Qy      241 GAAGATTCTGCACTTACTACTGTGACAGAGTTAGACATCCCGTACCTTTGGCCAG 300
Db      241 GAAGATTCTGCACTTACTACTGTGACAGAGTTAGACATCCCGTACCTTTGGCCAG 300
Qy      301 GGGACCAAGCTGGAGATCAA 321
Db      301 GGGACCAAGCTGGAGATCAA 321
```

```
RESULT 3
US-10-203-754A-61
; Sequence 61, Application US/10203754A
; Publication No. US20030157132A1
; GENERAL INFORMATION:
; APPLICANT: ITAMI, Seima
```

```
; APPLICANT: SEKI, Makoto
; APPLICANT: MATSURA, Yoshiharu
; APPLICANT: SHIBU, Tatsuro
; APPLICANT: YOTSUMOTO, Yoshihisa
; APPLICANT: MIYAMURA, Tatsuo
; TITLE OF INVENTION: Therapeutic Agent for Hepatitis C
; FILE REFERENCE: P22257
; CURRENT APPLICATION NUMBER: US/10/203,754A
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/JP01/00967
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-203-754A-61
```

```
Query Match      75.6%; Score 242.6; DB 15; Length 333;
Best Local Similarity 84.7%; Pred. No. 3.7e-73;
Matches 272; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy      1 GAGCTTCAGATGACCCAGTCTCCATCTCCCTGTGCTTGTGGAGACAGAGTCAAC 60
Db      1 GAGCTTCAGATGACCCAGTCTCCATCTCCCTGTGCTTGTGGAGACAGAGTCAAC 60
Qy      61 ATCACTTGTGGACAAAGTCAAGAGATTAAGCACTATTAATTTGGTATCAGAGAAACA 120
Db      61 ATCACTTGTGGACAAAGTCAAGAGATTAAGCACTATTAATTTGGTATCAGAGAAACA 120
Qy      121 GGAACGCTCTTAAGTGGCTCATTTACTGGCGATCTACCGGGAATCCGGGGTCCCTGAC 180
Db      121 GGAACGCTCTTAAGTGGCTCATTTACTGGCGATCTACCGGGAATCCGGGGTCCCTGAC 180
Qy      181 CGATTAGTGGACGGGGTCTGGGACAGATTTCATCTCAATCAGACAGTCTCAACCT 240
Db      181 AGTTCAAGTGGACGGGGTCTGGGACAGATTTCATCTCAATCAGACAGTCTCAACCT 240
Qy      241 GAAGATTCTGCACTTACTACTGTGACAGAGTTAGACATCCCGTACCTTTGGCCAG 300
Db      241 GAAGATTCTGCACTTACTACTGTGACAGAGTTAGACATCCCGTACCTTTGGCCAG 300
Qy      301 GGGACCAAGCTGGAGATCAA 321
Db      301 GGGACCAAGCTGGAGATCAA 321
```

```
RESULT 4
US-10-203-754A-65
; Sequence 65, Application US/10203754A
; Publication No. US20030157132A1
; GENERAL INFORMATION:
; APPLICANT: ITAMI, Seima
; APPLICANT: SEKI, Makoto
; APPLICANT: MATSURA, Yoshiharu
; APPLICANT: SHIBU, Tatsuro
; APPLICANT: YOTSUMOTO, Yoshihisa
; TITLE OF INVENTION: Therapeutic Agent for Hepatitis C
; FILE REFERENCE: P22257
; CURRENT APPLICATION NUMBER: US/10/203,754A
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/JP01/00967
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-203-754A-65
```

Query Match 75.6%; Score 242.6; DB 15; Length 900;
Best Local Similarity 84.7%; Pred. No. 5.3e-73;
Matches 212; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCCCTGCTGCTTCTGAGAGACAGAGTCAAC 60
DB 496 GACATGATATGACCCAGTCTCCATCCCTGCTGCTTCTGAGAGACAGAGTCAAC 555
QY 61 ATCACTTTCGCAAGTCAAGCATTTAGCATTTAAATTTGATACAGCAAAACA 120
DB 556 ATCACTTTCGCGGCAAGTCAAGCATTTAGCATTTAAATTTGATACAGCAAAACA 615
QY 121 GAGACACCTCTTAAGTGTCTCATTTACTGGCATTCACCCGGAATCCGGGTCCTGAC 180
DB 616 GGGAAAGCCCTTAAGTGTCTCATTTACTGGCATTCACCCGGAATCCGGGTCCTGAC 675
QY 181 CGATTGAGTGGACGGGCTTGGAGACAGATTTCATCTCCATCCATCAGAGTCAACCT 240
DB 676 AGTTCAAGTGGACGGGCTTGGAGACAGATTTCATCTCCATCAGAGTCAACCT 735
QY 241 GAAGATTTCGCACTTACTACTGTGACAGAGTTAGCAATCCGTAACCTTTGGCCAG 300
DB 736 GAAGATTTCGCACTTACTACTGTGACAGAGTTAGCAATCCGTAACCTTTGGCCAG 795
QY 301 GGGACCAAGCTGGAGATCAAA 321
DB 796 GGGACCAAGCTGGAGATCAAA 816

RESULT 5

US-09-848-798-199
; Sequence 199, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 199
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-848-798-199

Query Match 74.5%; Score 239.2; DB 10; Length 321;
Best Local Similarity 84.8%; Pred. No. 5.5e-72;
Matches 268; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 6 CCAGATGACCCAGTCTCCATCCCTGCTGCTTCTGAGAGACAGAGTCAACCTCA 65
DB 3 CGAGTCAACCCAGTCTCCATCCCTGCTGCTTCTGAGAGACAGAGTCAACCTCA 62
QY 66 TTGTGCGACAGTCAAGCATTTAGCATTTAAATTTGATACAGCAAAACAGAGCA 125
DB 63 TTGTGCGCGAGTCAAGCATTTAGCATTTAAATTTGATACAGCAAAACAGAGCA 122
QY 126 GCGCTTAAGTCTCATTTACTGGAGATTCACCGGAATCCGGGTCCTGACGATT 185
DB 123 AGCCCTTAAGTCTCATTTACTGGAGATTCACCGGAATCCGGGTCCTGACGATT 182
QY 186 CAGTGGCAGGGGTCTGAGACAGATTTCATCTCACCATCAGAGTCTCAACCTGAAG 245
DB 183 CAGTGGCAGGGGTCTGAGACAGATTTCATCTCACCATCAGAGTCTCAACCTGAAG 242

QY 246 TTCTGCACTTACTACTGTGACAGAGTTACGACATCCGTAACCTTTGGCCAGGGGAC 305
DB 243 TTCTGCACTTACTACTGTGACAGAGTTACGACATCCCTCACTTTTGGCCAGGGGAC 302
QY 306 CAGCTGGAGATCAAA 321
DB 303 CAGCTGGAGATCAAA 318

RESULT 6

US-10-203-754A-60
; Sequence 60, Application US/10203754A
; Publication No. US20030157132A1
; GENERAL INFORMATION:
; APPLICANT: ITAMI, Seima
; APPLICANT: MATSURA, Yoshiharu
; APPLICANT: SHIBUI, Tatsuro
; APPLICANT: YOSHIMOTO, Yoshihisa
; APPLICANT: MIYAMURA, Tatsuo
; TITLE OF INVENTION: Therapeutic Agent for Hepatitis C
; FILE REFERENCE: P22257
; CURRENT APPLICATION NUMBER: US/10/203,754A
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/JP01/00967
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-203-754A-60

Query Match 74.1%; Score 237.8; DB 15; Length 333;
Best Local Similarity 83.8%; Pred. No. 1.7e-71;
Matches 269; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCCCTGCTGCTTCTGAGAGACAGAGTCAAC 60
DB 1 GACATGATATGACCCAGTCTCCATCCCTGCTGCTTCTGAGAGACAGAGTCAAC 60
QY 61 ATCACTTTCGCAAGTCAAGCATTTAGCATTTAAATTTGATACAGCAAAACA 120
DB 61 ATCACTTTCGCGGCAAGTCAAGCATTTAGCATTTAAATTTGATACAGCAAAACA 120
QY 121 GAGACACCTCTTAAGTGTCTCATTTACTGGCATTCACCCGGAATCCGGGTCCTGAC 180
DB 121 GGGAAAGCCCTTAAGTGTCTCATTTACTGGCATTCACCCGGAATCCGGGTCCTGAC 180
QY 181 CGATTGAGTGGACGGGCTTGGAGACAGATTTCATCTCCATCAGAGTCAACCT 240
DB 181 AGTTCAAGTGGACGGGCTTGGAGACAGATTTCATCTCCATCAGAGTCAACCT 240
QY 241 GAAGATTTCGCACTTACTACTGTGACAGAGTTAGCAATCCGTAACCTTTGGCCAG 300
DB 241 GAAGATTTCGCACTTACTACTGTGACAGAGTTAGCAATCCGTAACCTTTGGCCAG 300
QY 301 GGGACCAAGCTGGAGATCAAA 321
DB 301 GGGACCAAGCTGGAGATCAAA 321

RESULT 7

US-10-203-754A-64
; Sequence 64, Application US/10203754A
; Publication No. US20030157132A1
; GENERAL INFORMATION:
; APPLICANT: ITAMI, Seima
; APPLICANT: SEKI, Makoto
; APPLICANT: MATSURA, Yoshiharu
; APPLICANT: SHIBUI, Tatsuro

APPLICANT: YOTSUMOTO, Yoshinisa
APPLICANT: MIYAMURA, Tatsuo
TITLE OF INVENTION: Therapeutic Agent for Hepatitis C
FILE REFERENCE: P22257
CURRENT APPLICATION NUMBER: US/10/203,754A
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: PCT/JP01/00967
PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn version 3.1
SEQ ID NO 64
LENGTH: 900
TYPE: DNA
ORGANISM: Homo sapiens
US-10-203-754A-64

Query Match 74.1%; Score 237.8; DB 15; Length 900;
Best Local Similarity 83.8%; Pred. No. 2,4e-71;
Matches 269; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Db 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTGCTTGTGGAGACAGAGTCACC 60
496 GACATCCAGATGACCCAGTCTCCATCTCCCTGCTGCTTGTGGAGACAGAGTCACC 555
QY 61 ATCACTTGGGAGCAAGTCAGAGCATTAGCAGCTATTAAATTGGTATCAGCAAAACCA 120
Db 556 ATCACTTGGGAGCAAGTCAGAGCATTAGCAGCTATTAAATTGGTATCAGCAAAACCA 615
QY 121 GGACAGCCTCTTAAGCTGCTCATTTCTGGCGATCAACCCGGGATCCGGGGTCCCTGAC 180
Db 616 GGGAAGCCCTTAAGCTGCTCATTTCTGGCGATCAACCCGGGATCCGGGGTCCCTGAC 675
QY 181 CGATTGAGTGGAGCGGGTCTGGGACAGATTTCACCTCAACATCAGAGTCACCACT 240
Db 676 AGTTGAGTGGAGCGGGTCTGGGACAGATTTCACCTCAACATCAGAGTCACCACT 735
QY 241 GAAGATTCTGCACTTCTACTGTCTGACAGAGTTAGCAACATCCCGTACCTTTGGCCAG 300
Db 736 GAAGATTCTGCACTTCTACTGTCTGACAGAGTTAGCAACATCCCGTACCTTTGGCCAG 795
QY 301 GGGACCAAGCTGAGATCAAA 321
Db 796 GGGACCAAGCTGAGATCAAA 816

RESULT 8
US-10-344-514-3
Sequence 3, Application US/10344514
Publication No. US20040120951A1
GENERAL INFORMATION:
APPLICANT: NAKASHIMA, Toshinori et al.
TITLE OF INVENTION: HUMAN ANTI-FACTOR VIII ANTIBODY
FILE REFERENCE: 0020-5111P
CURRENT APPLICATION NUMBER: US/10/344,514
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: JP 2001-177640
PRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 3
LENGTH: 324
TYPE: DNA
ORGANISM: Homo sapiens
US-10-344-514-3

Query Match 73.6%; Score 236.2; DB 17; Length 324;
Best Local Similarity 83.5%; Pred. No. 6e-71;
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTGCTTGTGGAGACAGAGTCACC 60
Db 1 GACATCCAGATGACCCAGTCTCCATCTCCCTGCTGCTTGTGGAGACAGAGTCACC 60
QY 61 ATCACTTGGGAGCAAGTCAGAGCATTAGCAGCTATTAAATTGGTATCAGCAAAACCA 120

Db 61 ATCACTTGGGAGCAAGTCAGAGCATTAGCAGCTATTAAATTGGTATCAGCAAAACCA 120
QY 121 GGACAGCCTCTTAAGCTGCTCATTTCTGGCGATCAACCCGGGATCCGGGGTCCCTGAC 180
Db 121 GGGAAGCCCTTAAGCTGCTCATTTCTGGCGATCAACCCGGGATCCGGGGTCCCTGAC 180
QY 181 CGATTGAGTGGAGCGGGTCTGGGACAGATTTCACCTTCAACATCAGAGTCACCACT 240
Db 181 AGTTGAGTGGAGCGGGTCTGGGACAGATTTCACCTTCAACATCAGAGTCACCACT 240
QY 241 GAAGATTCTGCACTTCTACTGTCTGACAGAGTTAGCAACATCCCGTACCTTTGGCCAG 300
Db 241 GAAGATTCTGCACTTCTACTGTCTGACAGAGTTAGCAACATCCCGTACCTTTGGCCAG 300
QY 301 GGGACCAAGCTGAGATCAAA 321
Db 301 GGGACCAAGCTGAGATCAAA 321

RESULT 9
US-10-344-514-4
Sequence 4, Application US/10344514
Publication No. US20040120951A1
GENERAL INFORMATION:
APPLICANT: NAKASHIMA, Toshinori et al.
TITLE OF INVENTION: HUMAN ANTI-FACTOR VIII ANTIBODY
FILE REFERENCE: 0020-5111P
CURRENT APPLICATION NUMBER: US/10/344,514
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: JP 2001-177640
PRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 4
LENGTH: 324
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(324)
US-10-344-514-4

Query Match 73.6%; Score 236.2; DB 17; Length 324;
Best Local Similarity 83.5%; Pred. No. 6e-71;
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTGCTTGTGGAGACAGAGTCACC 60
Db 1 GACATCCAGATGACCCAGTCTCCATCTCCCTGCTGCTTGTGGAGACAGAGTCACC 60
QY 61 ATCACTTGGGAGCAAGTCAGAGCATTAGCAGCTATTAAATTGGTATCAGCAAAACCA 120
Db 61 ATCACTTGGGAGCAAGTCAGAGCATTAGCAGCTATTAAATTGGTATCAGCAAAACCA 120
QY 121 GGACAGCCTCTTAAGCTGCTCATTTCTGGCGATCAACCCGGGATCCGGGGTCCCTGAC 180
Db 121 GGGAAGCCCTTAAGCTGCTCATTTCTGGCGATCAACCCGGGATCCGGGGTCCCTGAC 180
QY 181 CGATTGAGTGGAGCGGGTCTGGGACAGATTTCACCTTCAACATCAGAGTCACCACT 240
Db 181 AGTTGAGTGGAGCGGGTCTGGGACAGATTTCACCTTCAACATCAGAGTCACCACT 240
QY 241 GAAGATTCTGCACTTCTACTGTCTGACAGAGTTAGCAACATCCCGTACCTTTGGCCAG 300
Db 241 GAAGATTCTGCACTTCTACTGTCTGACAGAGTTAGCAACATCCCGTACCTTTGGCCAG 300
QY 301 GGGACCAAGCTGAGATCAAA 321
Db 301 GGGACCAAGCTGAGATCAAA 321

RESULT 10
US-09-192-854-1

```
; Sequence 1, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Method for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; EARLIER APPLICATION NUMBER: 60/066,729
; PRIOR FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-192-854-1

Query Match      73.6%; Score 236.2; DB 9; Length 720;
Best Local Similarity 83.5%; Pred. No. 8e-71;
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCCTCCTGCTCTTGTGGGAGACAGAGTCACC 60
   |||
DB 397 GACATCCAGATGACCCAGTCTCCATCCTCCTGCTCTTGTGGGAGACAGAGTCACC 456

QY 61 ATCACTTTCGCAAGTCAAGATGACAGATTAAGCACTATTAATTTGGATCAGAGAAACA 120
   |||
DB 457 ATCACTTTCGCGGCAAGTCAAGATGACAGATTAAGCACTATTAATTTGGATCAGAGAAACA 516

QY 121 GGAAGACCTCTTAAGTCTCATTTTACTGGGCACTACCCGGAAATCCGGGTCCTGAC 180
   |||
DB 517 GGGAAAGCCCCCTAAGCTCTCATTTTACTGGGCACTACCCGGAAATCCGGGTCCTGAC 576

QY 181 CGATTGAGTGGGCGGGGTCTGGGACAGATTTCACTTCACTCAGCATTCACCACT 240
   |||
DB 577 AGGTTCAGTGGGCGGGGTCTGGGACAGATTTCACTTCACTCAGCATTCACCACT 636

QY 241 GAAGATTCGCAACTTACTACTGTCAAGAGATTAAGCACTCCCTTGTGGCCAG 300
   |||
DB 637 GAAGATTTTCGCAACTTACTACTGTCAAGAGATTAAGCACTCCCTTGTGGCCAG 696

QY 301 GGGACCAAGCTGGAGATCAAA 321
   |||
DB 697 GGGACCAAGCTGGAGATCAAA 717

RESULT 11
US-09-968-561A-1
; Sequence 1, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 720
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-561A-1

Query Match      73.6%; Score 236.2; DB 9; Length 720;
Best Local Similarity 83.5%; Pred. No. 8e-71;
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCCTCCTGCTCTTGTGGGAGACAGAGTCACC 60
   |||
DB 397 GACATCCAGATGACCCAGTCTCCATCCTCCTGCTCTTGTGGGAGACAGAGTCACC 456

QY 61 ATCACTTTCGCAAGTCAAGATGACAGATTAAGCACTATTAATTTGGATCAGAGAAACA 120
   |||
DB 457 ATCACTTTCGCGGCAAGTCAAGATGACAGATTAAGCACTATTAATTTGGATCAGAGAAACA 516

QY 121 GGAAGACCTCTTAAGTCTCATTTTACTGGGCACTACCCGGAAATCCGGGTCCTGAC 180
   |||
DB 517 GGGAAAGCCCCCTAAGCTCTCATTTTACTGGGCACTACCCGGAAATCCGGGTCCTGAC 576

QY 181 CGATTGAGTGGGCGGGGTCTGGGACAGATTTCACTTCACTCAGCATTCACCACT 240
   |||
DB 577 AGGTTCAGTGGGCGGGGTCTGGGACAGATTTCACTTCACTCAGCATTCACCACT 636

QY 241 GAAGATTCGCAACTTACTACTGTCAAGAGATTAAGCACTCCCTTGTGGCCAG 300
   |||
DB 637 GAAGATTTTCGCAACTTACTACTGTCAAGAGATTAAGCACTCCCTTGTGGCCAG 696

QY 301 GGGACCAAGCTGGAGATCAAA 321
   |||
DB 697 GGGACCAAGCTGGAGATCAAA 717

RESULT 12
US-09-968-744A-1
; Sequence 1, Application US/09968744A
; Publication No. US20030148372A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073
; CURRENT APPLICATION NUMBER: US/09/968,744A
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-744A-1

Query Match      73.6%; Score 236.2; DB 10; Length 720;
Best Local Similarity 83.5%; Pred. No. 8e-71;
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCCTCCTGCTCTTGTGGGAGACAGAGTCACC 60
   |||
DB 397 GACATCCAGATGACCCAGTCTCCATCCTCCTGCTCTTGTGGGAGACAGAGTCACC 456

QY 61 ATCACTTTCGCAAGTCAAGATGACAGATTAAGCACTATTAATTTGGATCAGAGAAACA 120
   |||
DB 457 ATCACTTTCGCGGCAAGTCAAGATGACAGATTAAGCACTATTAATTTGGATCAGAGAAACA 516
```

QY 121 GGACAGCTCTCTAAGCTGCTCATTCTAGTGGCGATCTTACCAGGATCCGGGGTCCCTGAC 180
DB 517 GGGAAAGCCCCCTAAGCTCCTGATCTAGCTGATCCAGTTTGGAAGTGGGGTCCCATCA 576
QY 181 CGATTGAGTGGAGCGGGTCTGGGAGAGATTTCACTCTCACTCAGTCAAGTCAACCT 240
DB 577 AGGTCAGTGGGAGTGGATCTGGGAGAGATTTCACTCTCAGTCAAGTCAAGTCAACCT 636
QY 241 GAAGATTCTGCAACTTACTCTGTCAGCAGAGTTAGCAOATCCGTPACCTTTGGCCAG 300
DB 637 GAAGATTCTGCAACTTACTCTGTCAGCAGAGTTAGCAOATCCGTTAATGTTGGCCAA 696
QY 301 GGGACCAAGCTGGAGATCAA 321
DB 697 GGGACCAAGCTGGAAATCAA 717

RESULT 13
US-09-968-561A-1
; Sequence 1, Application US/09968561A
; Publication No. US20040038291A2
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-561A-1

Query Match 73.6%; Score 236.2; DB 11; Length 720;
Best Local Similarity 83.5%; Pred. No. 8e-71;
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTCTCTGTTGAGAGACAGATGAC 60
DB 397 GACATTCAGATGACCCAGTCTCCATCTCCCTGCTCTCTGTTGAGAGACAGATGAC 456
QY 61 ATCACTTGTGCGACAAGTCAAGACATTTAGACATTAATAATTGGTATCAGAGAAACA 120
DB 457 ATCACTTGTGCGCGGAGATGAGACATTTAGACATTAATAATTGGTATCAGAGAAACA 516
QY 121 GGAAGCTCTCTAAGCTGCTCAATTAAGTGGCAGATCAACCCGGGAATCCGGGGTCCCTGAC 180
DB 517 GGGAAAGCCCCCTAAGCTCCTGATCTATGCTGATCCAGTTGCAAAAGTGGGGTCCCATCA 576
QY 181 CGATTGAGTGGAGCGGGTCTGGGAGAGATTTCACTCTCACTCAGTCAAGTCAACCT 240
DB 577 AGGTCAGTGGGAGTGGATCTGGGAGAGATTTCACTCTCAGTCAAGTCAAGTCAACCT 636
QY 241 GAAGATTCTGCAACTTACTCTGTCAGCAGAGTTAGCAOATCCGTPACCTTTGGCCAG 300
DB 637 GAAGATTCTGCAACTTACTCTGTCAGCAGAGTTAGCAOATCCGTTAATGTTGGCCAA 696
QY 301 GGGACCAAGCTGGAGATCAA 321
DB 697 GGGACCAAGCTGGAAATCAA 717

DB 697 GGGACCAAGCTGGAAATCAA 717

RESULT 14
US-10-744-774-2
; Sequence 2, Application US/10744774
; Publication No. US20040219643A1
; GENERAL INFORMATION:
; APPLICANT: Domantis Limited
; APPLICANT: Medical Research Council
; APPLICANT: Ignatovich, Olga
; APPLICANT: Jones, Philip C.
; APPLICANT: Tomlinson, Ian
; APPLICANT: Winter, Greg
; TITLE OF INVENTION: Dual Specific Ligand
; FILE REFERENCE: 8039/2102
; CURRENT APPLICATION NUMBER: US/10/744,774
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: PCT/GB02/03014
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: GB 0115841.9
; PRIOR FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH/HS A
US-10-744-774-2

Query Match 73.6%; Score 236.2; DB 18; Length 720;
Best Local Similarity 83.5%; Pred. No. 8e-71;
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTCTCTGTTGAGAGACAGATGAC 60
DB 397 GACATTCAGATGACCCAGTCTCCATCTCCCTGCTCTCTGTTGAGAGACAGATGAC 456
QY 61 ATCACTTGTGCGACAAGTCAAGACATTTAGACATTAATAATTGGTATCAGAGAAACA 120
DB 457 ATCACTTGTGCGCGGAGATGAGACATTTAGACATTAATAATTGGTATCAGAGAAACA 516
QY 121 GGAAGCTCTCTAAGCTGCTCAATTAAGTGGCAGATCAACCCGGGAATCCGGGGTCCCTGAC 180
DB 517 GGGAAAGCCCCCTAAGCTCCTGATCTATGCTGATCCAGTTGCAAAAGTGGGGTCCCATCA 576
QY 181 CGATTGAGTGGAGCGGGTCTGGGAGAGATTTCACTCTCAGTCAAGTCAACCT 240
DB 577 AGGTCAGTGGGAGTGGATCTGGGAGAGATTTCACTCTCAGTCAAGTCAAGTCAACCT 636
QY 241 GAAGATTCTGCAACTTACTCTGTCAGCAGAGTTAGCAOATCCGTPACCTTTGGCCAG 300
DB 637 GAAGATTCTGCAACTTACTCTGTCAGCAGAGTTAGCAOATCCGTTAATGTTGGCCAA 696
QY 301 GGGACCAAGCTGGAGATCAA 321
DB 697 GGGACCAAGCTGGAAATCAA 717

RESULT 15
US-09-848-798-113
; Sequence 113, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rb(D)-BINDING PROTEIN AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 06:11:35 ; Search time 1873.31 Seconds
(without alignments)
6244.126 Million cell updates/sec

Title: US-09-403-107-141

Perfect score: 321
Sequence: 1 gagcccccagatgacccacgac.....ggacccaagctggagatcaaa 321

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapect 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	244.2	76.1	624	6	CD690145 EST6668 h
2	243.4	75.8	921	4	BG341239 602463904
3	242.6	75.6	487	2	AM405301 UI-HF-BLO
4	241	75.1	525	6	CD705928 EST22455
5	239.4	74.6	447	2	AM405752 UI-HF-BLO
6	238.6	74.3	608	2	AM404714 UI-HF-BLO
7	237.8	74.1	854	5	BX397739 BX397739
8	237.8	74.1	422	2	AM407904 UI-HF-BLO
9	236.2	73.6	311	4	AM404992 UI-HF-BLO
10	236.2	73.6	671	2	BM830977 K-EST104
11	236.2	73.6	684	4	BM769909 K-EST053
12	236.2	73.6	693	6	CD684441 EST961 hu
13	236.2	73.6	742	6	CB984723 AGENCOURT
14	236.2	73.6	754	6	CB986767 AGENCOURT
15	236.2	73.6	762	6	CB9858057 AGENCOURT
16	236.2	73.6	762	6	CB9858057 AGENCOURT
17	236.2	73.6	762	6	CB9858057 AGENCOURT
18	234.6	73.1	493	2	AM405753 UI-HF-BLO
19	234.6	73.1	532	4	BM823145 K-EST094
20	234.6	73.1	550	6	CD709957 EST26484
21	233.8	72.8	785	6	CB986236 AGENCOURT
22	233.8	72.8	390	5	BX956603 DXFZP781B
23	233.8	72.8	1084	6	CB986592 AGENCOURT
24	233	72.6	431	2	AM406886 UI-HF-BLO

25	233	72.6	750	6	CB985395 AGENCOURT
26	232.2	72.3	807	6	CB958380 AGENCOURT
27	231.6	72.1	868	5	BX397738 BX397738
28	231.4	72.1	499	4	BM823529 K-EST0094
29	231.4	72.1	499	6	CD685478 EST1998 h
30	231.4	72.1	543	6	CD687669 EST4190 h
31	231.4	72.1	566	2	AM406081 UI-HF-BLO
32	231.4	72.1	677	4	BG398225 602440072
33	231.4	72.1	837	6	CB984807 AGENCOURT
34	231.4	72.1	864	4	BG548281 602575248
35	230.4	71.8	937	5	BQ706234 AGENCOURT
36	229.8	71.6	444	5	BX956113 DXFZP781C
37	229.8	71.6	460	2	AM405906 UI-HF-BLO
38	229.8	71.6	471	2	AM406294 UI-HF-BLO
39	229.8	71.6	619	6	CD693603 EST10126
40	229.8	71.6	715	6	CB986379 AGENCOURT
41	229.8	71.6	724	6	CB959008 AGENCOURT
42	229.8	71.6	725	6	CB987519 AGENCOURT
43	229.8	71.6	738	6	CB987788 AGENCOURT
44	229.8	71.6	745	6	CB985128 AGENCOURT
45	229.8	71.6	797	6	CB987347 AGENCOURT

ALIGNMENTS

RESULT 1
CD690145 624 bp mRNA linear EST 25-JUN-2003
LOCUS EST6668 human nasopharynx Homo sapiens cDNA, mRNA sequence.
DEFINITION CD690145
ACCESSION CD690145
VERSION CD690145.1 GI:32210615
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 624)
Zeng,Y.-X., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Liu,X.-Q.

AUTHORS Transcriptional Gene Expression Profile of Human Nasopharynx

JOURNAL Unpublished (2003)

COMMENT Contact: Yixin Zeng

Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.

FEATURES
source Location/Qualifiers
1..624
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/rfeature_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Query Match 76.1%; Score 244.2; DB 6; Length 624;
Best Local Similarity 85.0%; Pred. No. 8.1e-66;
Matches 273; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 1 GAGCTCCAGATGACGAGTCTCCATCTCTGCTTCTGTTGGAGACAGAGTACC 60
DB 114 GAGATCCAGATGACGAGTCTCCATCTCTGCTTCTGATCTGTAGAGACAGAGTACC 173
QY 61 ATCACTTGTGGAAGAGTACGAGCATTTAAATTTGTTATGACGAGAAACCA 120
DB 174 ATCACTTGTGGAAGAGTACGAGCATTTAAATTTGTTATGACGAGAAACCA 233
QY 121 GAGACCTCTTAAGTGTCTATTCTGCGCATTCACCGGGAATCCGGGGTCCCTGAC 180

Db 234 GGGAAAGCCCTTAGCTCCGATCTATGTCGATCCAGTTTGCAAGTGGGGTCCCATCA 293
QY 181 CGATTCAGTGGCAGCGGGTCTGGAGACAGATTTCACCTCTCCATCCATCAGAGTCTACAACCT 240
Db 294 AGATTGAGTGGCAGTGGATCTGGAGACAGATTTCACCTCTCCATCCATCAGAGTCTACAACCT 353
QY 241 GAAGATTCTGCACCTACTACTGTCTCAGCAGAGTTTACGACATCCCGTACACTTTTGGCCAG 300
Db 354 GAAGATTCTGCACCTACTACTGTCTCAGCAGAGTTTACGACATCCCGTACACTTTTGGCCAG 413
QY 301 GGGACCAAGCTGGAGATCAAA 321
Db 414 GGGACCAAGCTGGAGATCAAA 434

RESULT 2
BG341239 921 bp mRNA linear EST 27-FEB-2001
LOCUS 602463904F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4576560 5',
DEFINITION mRNA sequence.
ACCESSION BG341239
VERSION BG341239.1 GI:13147677
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
1 (bases 1 to 921)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM1289 row: h column: 01
High quality sequence stop: 732.
Location/Qualifiers
1..921
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4576560"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

ORIGIN
Query Match 75.8%; Score 243.4; DB 4; Length 921;
Best Local Similarity 86.9%; Pred. No. 1.6e-65;
Matches 279; Conservative 0; Mismatches 41; Indels 1; Gaps 1;
QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTCTGCTTGTGGAGACAGAGTCAAC 60
Db 81 GACATTCAGATGACCCAGTCTCCATCTCCCTGTCTGCTTGTGGAGACAGAGTCAAC 140
QY 61 ATCACTTGTGGACAAAGTCAGAGCATTAAGCATTAATAATTGGTATCAGAGAAACCA 120

Db 141 ATCACTTGTGGCGGACAGTCAAGCATTTAGACACTATTATTAATTGGTATCAGAGAAACCA 200
QY 121 GGAAGCCCTCTTAAGTGTCTCATTTTATCTGGCGATCTACCCGGAAATCCGGGGTCCCTGAC 180
Db 201 GGAAGAGCC-CCTAAGTCTCTGATCTATGCTGTGATCCAGATTTCAGAAAGTGGGCTCCATCA 259
QY 181 CGATTCAGTGGCAGCGGGTCTGGAGACAGATTTCACCTCTCCATCCATCAGAGTCTACAACCT 240
Db 260 AGATTGAGTGGCAGTGGATCTGGAGACAGATTTCACCTCTCCATCCATCAGAGTCTACAACCT 319
QY 241 GAAGATTCTGCACCTACTACTGTCTCAGCAGAGTTTACGACATCCCGTACACTTTTGGCCAG 300
Db 320 GAAGATTCTGCACCTACTACTGTCTCAGCAGAGTTTACGACATCCCGTACACTTTTGGCCAG 379
QY 301 GGGACCAAGCTGGAGATCAAA 321
Db 380 GGGACCAAGCTGGAGATCAAA 400

RESULT 3
AM405301 487 bp mRNA linear EST 16-FEB-2000
LOCUS UI-HF-BL0-ack-b-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
DEFINITION IMAGE:3059259 5', mRNA sequence.
ACCESSION AM405301
VERSION AM405301.1 GI:6924358
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
1 (bases 1 to 487)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbip/image/image.html
Seq primer: M13 Forward.
Location/Qualifiers
1..487
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3059259"
/tissue_type="lymph"
/tissue_type="germinal center B cells"
/cell_type="MGC85"
/lab_host="DH10B (LTJ)"
/clone_lib="NIH_MGC_37"
/note="Vector: pRT3-Pac; Site 1: NotI; Site 2: Eco RI;
constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN
Query Match 75.6%; Score 242.6; DB 2; Length 487;
Best Local Similarity 84.7%; Pred. No. 2.4e-65;
Matches 272; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTCTGCTTGTGGAGACAGAGTCAAC 60
Db 42 GACATTCAGATGACCCAGTCTCCATCTCCCTGTCTGCTTGTGGAGACAGAGTCAAC 101
QY 61 ATCACTTGTGGACAAAGTCAGAGCATTTAGACACTTAATAATTGGTATCAGAGAAACCA 120

Db 102 ATACCTTCCGGGCAATCAGACATTAGACCTATTAAATGGTATCAGCAAGAAACCA 161
QY 121 GAGACGCTCTTAAGCTGCTCATTTACTGGAGATCAACCGGAATCCGGGATCCCTGAC 180
Db 162 GGGAAAGCCCTTATCTCTGATTTATGTCATTCATCCATTTTGGAAAGTGGGGTCCCATCA 221
QY 181 CGATTAGTGGCAGCGGGTCTGGAGACGATTTTCACTCTCAGCATCAGACATCTACAACT 240
Db 222 AGGTTCAGTGGCAGTGTGATCTGGAGCAATTTCACTCTCAGCATCAGACATCTGCAACT 281
QY 241 GAAGATTTCTCACTTACTACTGTGACAGATTTAGACATCCGTCACATTTTGGCCAG 300
Db 282 GAAGATTTTCTCACTTACTACTGTGACAGATTTAGACATCCGTCAGTCCCGTACATTTGGCCAG 341
QY 301 GGGACCAAGCTGGAGATCAAA 321
Db 342 GGGACCAAGCTGGAGATCAAA 362

RESULT 4
LOCUS CD705928 525 bp mRNA linear EST 25-JUN-2003
DEFINITION EST22455 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD705928
VERSION CD705928.1 GI:32236558
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 525)
Zeng,Y.-X.
Transcriptional Gene Expression Profile of Human Nasopharynx
Unpublished (2003)
Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@zsuns.edu.cn.

FEATURES
source
Location/Qualifiers
1..525
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN
Query Match 75.1%; Score 241; DB 6; Length 525;
Best Local Similarity 84.4%; Pred. No. 7.9e-65;
Matches 271; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Db 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTCTCTCTGGAGAGACAGATCACC 60
QY 117 GACATCCAGATGACCCAGTCTCCATCTCCCTGCTCTCTGGAGAGACAGATCACC 176
Db 61 ATCACTTTCGGAACAAGTCAAGCATTAGAGAGCTATTAAATGGTATCAGCAAGAAACCA 120
QY 177 ATCACTTTCGGAACAAGTCAAGCATTAGAGAGCTATTAAATGGTATCAGCAAGAAACCA 236
Db 121 GGAAGCTCTTAAGCTGCTCATTTACTGGAGATTTAGACATCCGGGAATCCGGGATCCCTGAC 180
QY 237 GGGAAAGCCCTTATCTCTGATTTATGTCATTCATCCATTTTGGAAAGTGGGGTCCCATCA 296
Db 181 CGATTAGTGGCAGCGGGTCTGGAGACGATTTTCACTCTCAGCATCAGACATCTACAACT 240
QY 297 AGGTTCAGTGGCAGTGTGATCTGGAGCAATTTCACTCTCAGCATCAGACATCTGCAACT 356

QY 241 GAAGATTTCTCACTTACTACTGTGACAGATTTAGACATCCGTCACATTTTGGCCAG 300
Db 357 GAAGATTTTCTCACTTACTACTGTGACAGATTTAGACATCCGTCACATTTTGGCCAG 416
QY 301 GGGACCAAGCTGGAGATCAAA 321
Db 417 GGGACCAAGCTGGAGATCAAA 437

RESULT 5
LOCUS AM405752 447 bp mRNA linear EST 16-FEB-2000
DEFINITION UI-HF-BL0-abp-a-01-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3057288 5', mRNA sequence.
ACCESSION AM405752
VERSION AM405752.1 GI:6924809
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 447)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Straube, Ph.D.
Email: cgaabs-r@mail.nih.gov
Rco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/BLNL at:
www-bio.lnl.gov/biopr/image/image.html
Seq primer: M13 Forward.

FEATURES
source
Location/Qualifiers
1..447
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3057288"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LT1)"
/lab_host="NIH MGC 37"
/note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN
Query Match 74.6%; Score 239.4; DB 2; Length 447;
Best Local Similarity 84.1%; Pred. No. 2.4e-64;
Matches 270; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Db 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTCTCTCTGGAGAGACAGATCACC 60
QY 83 GACATCCAGATGACCCAGTCTCCATCTCCCTGCTCTCTGGAGAGACAGATCACC 142
Db 61 ATCACTTTCGGAACAAGTCAAGCATTAGAGAGCTATTAAATGGTATCAGCAAGAAACCA 120
QY 143 ATCACTTTCGGAACAAGTCAAGCATTAGAGAGCTATTAAATGGTATCAGCAAGAAACCA 202
Db 121 GGAAGCTCTTAAGCTGCTCATTTACTGGAGATTTAGACATCCGGGAATCCGGGATCCCTGAC 180
QY 203 GGGAAAGCCCTTATCTCTGATTTATGTCATTCATCCATTTTGGAAAGTGGGGTCCCATCA 262
Db 181 CGATTAGTGGCAGCGGGTCTGGAGACGATTTTCACTCTCAGCATCAGACATCTACAACT 240

Db 263 ACCTGAGTGGAGTGGATCTGGAGACAGATTTCACTCTACATCAGACAGTCTGCAACT 322
 QY 241 GAAGATTTCGAACCTTACTCTGTCAAGAGATTACAGATCCGTACACTTTTGGCCAG 300
 Db 323 GAAGATTTCGAACCTTACTCTGTCAAGAGATTACAGATCCGTACACTTTTGGCCAG 382
 QY 301 GGGACCAAGCTGGAGATCAAA 321
 Db 383 GGGACCAAGCTGGAGATCAAA 403

RESULT 6

AM404714

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

608 bp mRNA linear EST 16-FEB-2000
 UT-HR-BL0-acd-c-11-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
 IMAGE:3058580 5', mRNA sequence.
 AM404714
 AM404714.1 GI:6923771
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
 1 (bases 1 to 608)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLN at:
 www-bio.lnl.gov/dbip/image/image.html
 Seq primer: M13 Forward.
 Location/Qualifiers

FEATURES

source

1..608
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3058580"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="NIH MGC 37"
 /clone_id="NIH MGC 37"
 /note="Vector: pTZ19-Pac; Site 1: NotI; Site 2: Eco RI;
 constructed from size fractionated cytoplasmic mRNA
 (1.5-2.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match

Best Local Similarity

Matches

74.3%; Score 238.6; DB 2; Length 608;
 84.5%; Pred. No. 4,7e-64;
 268; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 5 TCCAGATGACCAAGTCTCCATCTCCCTGCTCTGTCTGTGGAGACAGAGTACCATCA 64
 Db 46 TCCAGATGACCAAGTCTCCATCTCCCTGCTCTGTGTAGAGACAGAGTACCATCA 105
 QY 65 CTGTGCGACAGTACAGAGATTTAGAGATTAATAATTGGTATCAAGCAAGAACAGAC 124
 Db 106 CTGTGCGCGGACAGTACAGAGATTTAGAGATTAATAATTGGTATCAAGCAAGAACAG 165
 QY 125 AGCCTCTAAGCTGCTCACTTACTGGGAGATCAACCGGGAATCCGGGGTCCCTGACCAT 184
 Db 166 AAGCCCTTAAGCTGCTCACTTACTGGGAGATCAACCGGGAATCCGGGGTCCCTGACCAT 225
 QY 185 TCAGTGGAGCGGGTCTGGGACAGATTTCACTCTACCATGACAGTCTACAACCTGAAG 244

Db 226 TCAGTGGAGCGGGTCTGGGACAGATTTCACTCTACCATGACAGTCTACAACCTGAAG 285
 QY 245 ATTCTGCAACTTACTACTGTCAAGAGATTACAGATCCGTACACTTTTGGCCAGGGA 304
 Db 286 ATTCTGCAACTTACTACTGTCAAGAGATTACAGATCCGTACACTTTTGGCCAGGGA 345
 QY 305 CCAAGCTGGAGATCAAA 321
 Db 346 CCAAGCTGGAGATCAAA 362

RESULT 7

BX397739

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

854 bp mRNA linear EST 28-APR-2004
 BX397739 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0D1041YP06 5-PRIME, mRNA sequence.
 BX397739
 BX397739.2 GI:46847409
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
 1 (bases 1 to 854)
 Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 13, 2003 this sequence version replaced gi:30617375.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 1696.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?cs=CS0D1041DH03QP1&c=1696.r.

FEATURES

source

1..854
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1041YP06"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match

Best Local Similarity

Matches

74.1%; Score 238; DB 5; Length 854;
 85.7%; Pred. No. 8.1e-64;
 276; Conservative 0; Mismatches 45; Indels 1; Gaps 1;

QY 1 GAGCTCCAGATGACCAAGTCTCCATCTCCCTGCTCTGTCTGTGGAGACAGAGTACCC 60
 Db 14 GAGCTCCAGATGACCAAGTCTCCATCTCCCTGCTCTGTCTGTGGAGACAGAGTACCC 73
 QY 61 ATCACTTGTGGACAGTACAGAGATTTAGAGATTAATAATTGGTATCAAGCAAGAACCA 120
 Db 74 ATCACTTGTGGACAGTACAGAGATTTAGAGATTAATAATTGGTATCAAGCAAGAACCA 133
 QY 121 GAGAGCTCTAAGCTGCTCACTTACTGGGAGATCAACCGGGAATCCGGGGTCCCTGAC 180
 Db 134 GGGAAAGCTCTAAGCTGCTCACTTACTGGGAGATCAACCGGGAATCCGGGGTCCCTGAC 193
 QY 181 CGATTCACTGAGCGGGTCTGGGACAGATTTCACTCTACCATGACAGTCTACAACCTGA 240

Db 194 AGGTCAGTGGCAGTGGATCTGGGACAGATTTCATCTCAGCATCAGAGCTTCCAACT 253
 QY 241 GAAGATT-CTGCACTTACTACTGTGACAGAGTTACGACATCCGTACCTTTGGCCA 299
 Db 254 GAAGATTATGCACTTACTACTGTGACAGAGTTACGATCCCGTACCTTTGGCCA 313
 QY 300 GGGGACCAAGCTGGAGATCAAA 321
 Db 314 GGGGACCAAGCTGGAGATCAAA 335

RESULT 8

AM407904

LOCUS 422 bp mRNA linear EST 16-FEB-2000
 DEFINITION UI-HF-BL0-add-a-01-0-UI-r2 NIH_MGC_37 Homo sapiens cDNA clone
 IMAGE:3061128 5', mRNA sequence.

ACCESSION

AM407904

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 1 (bases 1 to 422)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/dbp/image/image.html
 Seq primer: M13 Forward.

FEATURES

source

Location/Qualifiers

1..422
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3061128"
 /issue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LTI)"
 /clone_lib="NIH_MGC_37"
 /note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (1.5-2.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 74.1%; Score 237.8; DB 2; Length 422;
 Best Local Similarity 83.8%; Pred. No. 7.6e-64;

Matches 269; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 GAGCTCAGATGACCCAGTCTCATCTCCCTGCTTCTTGTGGAGACAGAGTCAAC 60
 Db 23 GACATCAATGACCCAGTCTCATCTCCCTGCTTGTGGAGACAGAGTCAAC 82
 QY 61 ATCACTTGTGCAAGTCAAGATTAAGAGCTATTAATTTGATCAGAGAAACA 120
 Db 83 ATCACTTGTGCAAGTCAAGATTAAGAGCTATTAATTTGATCAGAGAAACA 142
 QY 121 GGAAGACCTCTTAAGTCTCATTTACTGGCATTTACCCGGGAATCCGGGTCCTGAC 180
 Db 143 GGAAGACCTCTTAAGTCTCATTTACTGGCATTTACCCGGGAATCCGGGTCCTGAC 202
 QY 181 CGATTAGTGGCAGCGGGTCTGGGACAGATTTCATCTCAGCATCAGAGTCAACCT 240

Db 203 AGGTCAGTGGCAGTGGATCTGGGACAGATTTCATCTCAGCATCAGAGCTTCCAACT 262
 QY 241 GAAGATTCTGCACTTACTACTGTGACAGAGTTACGACATCCGTACCTTTGGCCA 300
 Db 263 GAAGATTATGCACTTACTACTGTGACAGAGTTACGATCCCGTACCTTTGGCCA 322
 QY 301 GGGGACCAAGCTGGAGATCAAA 321
 Db 323 GGGGACCAAGCTGGAGATCAAA 343

RESULT 9

AM404992

LOCUS 391 bp mRNA linear EST 16-FEB-2000
 DEFINITION UI-HF-BL0-abx-a-03-0-UI-r1 NIH_MGC_37 Homo sapiens cDNA clone
 IMAGE:3058060 5', mRNA sequence.

ACCESSION

AM404992

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 1 (bases 1 to 391)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/dbp/image/image.html
 Seq primer: M13 Forward.

Location/Qualifiers
 1..391
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3058060"
 /issue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LTI)"
 /clone_lib="NIH_MGC_37"
 /note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (1.5-2.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 73.6%; Score 236.2; DB 2; Length 391;
 Best Local Similarity 83.5%; Pred. No. 2.4e-63;

Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 GAGCTCAGATGACCCAGTCTCATCTCCCTGCTTCTTGTGGAGACAGAGTCAAC 60
 Db 65 GACATCAATGACCCAGTCTCATCTCCCTGCTTGTGGAGACAGAGTCAAC 124
 QY 61 ATCACTTGTGCAAGTCAAGATTAAGAGCTATTAATTTGATCAGAGAAACA 120
 Db 125 ATCACTTGTGCAAGTCAAGATTAAGAGCTATTAATTTGATCAGAGAAACA 184
 QY 121 GGAAGACCTCTTAAGTCTCATTTACTGGCATTTACCCGGGAATCCGGGTCCTGAC 180
 Db 185 GGAAGACCTCTTAAGTCTCATTTACTGGCATTTACCCGGGAATCCGGGTCCTGAC 244

QY 181 CGATTTCAGTGGACGCGGCTCTGGGACAGATTTCACCTCTCAGCATCAGAGCTCTACACCT 240
 DB 245 AGGTTGAGTGGCAGTGGATCTGGGACAGATTTCACCTCTCAGCATCAGAGCTCTACACCT 304
 QY 241 GAAGATTCTGCACTTACTACTGTCGAGAGTTCAGATATCCCGTACCTTTGGCCAG 300
 DB 305 GAAGATTCTGCACTTACTACTGTCGAGAGTTCAGATATCCCGTACCTTTGGCCAG 364
 QY 301 GGGACCAAGCTGGAGATCAAA 321
 DB 365 GGGACCAAGCTGGAGATCAAA 385
 RESULT 10
 BM830977 671 bp mRNA linear EST 06-MAR-2002
 LOCUS K-EST00104754 S14K402s1 Homo sapiens cDNA clone S14K402s1-20-E05 5',
 DEFINITION mRNA sequence.
 ACCESSION BM830977 GI:19187386
 VERSION BM830977.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 671)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)
 CONTACT: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 20 row: E column: 05
 High quality sequence stop: 671.
 Location/Qualifiers
 1..671
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S14K402s1-20-E05"
 /cell_line="K402"
 /lab_host="Top10F"
 /clone_1ib="S14K402s1"
 /note="Organ: Stomach; Vector: pTZ19RP1; Site_1: EcoRI;
 Site_2: NotI; The poly (A) + RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then deacapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker. The decapped
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dT-selected mRNA by
 priming with dT-tailed vector. The dT-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library. After analyzing and
 sequencing about 2,000 ~ 3,000 colonies in original cDNA
 library, the abundant cDNAs were selected and amplified by
 PCR reaction using vector region primer including T7
 promoter as 5' primer and N(dT)14 as 3' primer. The PCR
 products were used as template for synthesis of
 biotinylated single stranded RNA by in vitro transcription
 reaction. The synthesized RNA probes were hybridized with
 antisense single stranded cDNAs prepared from original

library and incubated with avidin-gel. After removing
 DNA-RNA hybrids by centrifuge, the subtracted cDNA
 libraries were constructed by transformation of the
 remaining DNA into competent cells E. coli Top10F with
 electroporation method."

ORIGIN
 Query Match 73.6%; Score 236.2; DB 4; Length 671;
 Best local similarity 83.5%; Pred. No. 2.8e-63;
 Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCCCTCCCTGCTGCTTGGGAGACAGATCACC 60
 DB 90 GACATCCAGATGACCCAGTCTCCATCCCTCCCTGCTGCTTGGGAGACAGATCACC 149
 QY 61 ATCACTTGTGCGACAGTTCAGAGCATTTAGAGCTATTTAAATGGTATCAGCAAAACA 120
 DB 150 ATCGCTTCCCGGCGAGTTCAGAGCATTTAGAGCTATTTAAATGGTATCAGCAAAACA 209
 QY 121 GACAGCCTCTTAACTGCTCATTTTACTGCGGATTCACCCGGGAATCCGGGGTCCCTGAC 180
 DB 210 GGGAGAGCCCTTAACTGCTCATTTTACTGCGGATTCACCCGGGAATCCGGGGTCCCTGAC 269
 QY 181 CGATTTCAGTGGACGCGGCTCTGGGACAGATTTCACCTCTCAGCATCAGAGCTCTACACCT 240
 DB 270 AGGTTGAGTGGCAGTGGATCTGGGACAGATTTCACCTCTCAGCATCAGAGCTCTACACCT 329
 QY 241 GAAGATTCTGCACTTACTACTGTCGAGAGTTCAGATATCCCGTACCTTTGGCCAG 300
 DB 330 GAAGATTCTGCACTTACTACTGTCGAGAGTTCAGATATCCCGTACCTTTGGCCAG 389
 QY 301 GGGACCAAGCTGGAGATCAAA 321
 DB 390 GGGACCAAGCTGGAGATCAAA 410

RESULT 11
 BM769909 684 bp mRNA linear EST 04-MAR-2002
 LOCUS K-EST0053259 S14K402 Homo sapiens cDNA clone S14K402-24-C07 5',
 DEFINITION mRNA sequence.
 ACCESSION BM769909
 VERSION BM769909.1 GI:19099524
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 684)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)
 CONTACT: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 24 row: C column: 07
 High quality sequence stop: 684.
 Location/Qualifiers
 1..684
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S14K402-24-C07"
 /cell_line="K402"
 /lab_host="Top10F"
 /clone_1ib="S14K402"
 /note="Organ: Stomach; Vector: pTZ19RP1; Site_1: EcoRI;

Site 2: NotI: The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then deapped with labacco acid pyrophosphatase (LAP). The deapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoR I which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 73.6%; Score 236.2; DB 4; Length 684;
Best Local Similarity 83.5%; Pred. No. 2.8e-63;
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTCTGCTTGTGGAGACAGAGTCACC 60
DB 90 GACATCCAGATGACCCAGTCTCCATCTCCCTGCTCTGCTTGTGGAGACAGAGTCACC 149
QY 61 ATCACTTGTGCGAAGTCAGAGCATTTAGAGCTATTTAAATTGGTATCAGCAAAACCA 120
DB 150 ATGCTTGTGCGGCGGCAAGTCAGAGCATTTATTTAAATTGGTATCAGCAAAACCA 209
QY 121 GAGACGCTCTTAAGTGTCTATTTACTGGCGATCTACCGGGAATCCGGGGTCCCTGAC 180
DB 210 GGGAGAGCCCCCTTAAGTGTCTATTTACTGGCGATCTACCGGGAATCCGGGGTCCCTGAC 269
QY 181 CGATTCAGTGGCAGCGGGTCTGGAGACAGATTTCACTCTCACATCAGAGTCACACCT 240
DB 270 AGGTTAGTGGCAGTGGATCTGGAGACAGATTTCACTCTCACATCAGAGTCACACCT 329
QY 241 GAAGATTTGCAACTTACTGTCTGACAGAGTTAGACATCCCGTACACTTTTGGCCAG 300
DB 330 GAAGATTTTGGCACTTACTGTCTGCAACAGAGTTAGACATCCCGTACACTTTTGGCCAG 389
QY 301 GGGACCAAGCTGAGATCAAA 321
DB 390 GGGACCAAGCTGAGATCAAA 410

RESULT 12
CD684441 693 bp mRNA linear EST 25-JUN-2003
DEFINITION EST961 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD684441
VERSION CD684441.1 GI:32199435
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 693)
Liu X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.

TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@zsums.edu.cn.

FEATURES
source 1. .693
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Query Match 73.6%; Score 236.2; DB 6; Length 693;
Best Local Similarity 83.5%; Pred. No. 2.8e-63;
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTCTGCTTGTGGAGACAGAGTCACC 60
DB 120 GACATCCAGATGACCCAGTCTCCATCTCCCTGCTCTGCTTGTGGAGACAGAGTCACC 179
QY 61 ATCACTTGTGCGAAGTCAGAGCATTTAGAGCTATTTAAATTGGTATCAGCAAAACCA 120
DB 180 ATCACTTGTGCGGCGGCAAGTCAGAGCATTTAGCCGCTATTTAAATTGGTATCAGCAAAACCA 239
QY 121 GAGACGCTCTTAAGTGTCTATTTACTGGCGATCTACCGGGAATCCGGGGTCCCTGAC 180
DB 240 GGGAAAGCCCCCTTAAGTGTCTATTTACTGGCGATCTACCGGGAATCCGGGGTCCCTGAC 299
QY 181 CGATTCAGTGGCAGCGGGTCTGGAGACAGATTTCACTCTCACATCAGAGTCACACCT 240
DB 300 AGGTTAGTGGCAGTGGATCTGGAGACAGATTTCACTCTCACATCAGAGTCACACCT 359
QY 241 GAAGATTTGCAACTTACTGTCTGACAGAGTTAGACATCCCGTACACTTTTGGCCAG 300
DB 360 GAAGATTTTGGCACTTACTGTCTGCAACAGAGTTAGACATCCCGTACACTTTTGGCCAG 419
QY 301 GGGACCAAGCTGAGATCAAA 321
DB 420 GGGACCAAGCTGAGATCAAA 440

RESULT 13
CB984723 742 bp mRNA linear EST 01-MAY-2003
DEFINITION AGENCOURT 13460684 NIH-MGC_184 Homo sapiens cDNA clone
ACCESSION CB984723
VERSION CB984723
KEYWORDS IMAGE:30325808 5', mRNA sequence.
SOURCE EST.
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE NIH-MGC
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLOUTIER Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov

Plate: NDCM132 row: d column: 09
High quality sequence stop: 453.
Location/Qualifiers
1. .742
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30325808"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH-MGC 184"
/note="Organ: Pooled-glandular; Vector: pDNR-LIB; Site_1: SfiI (ggcattatggcc); Site_2: SfiI (ggcgctctggcc);

FEATURES

source 1. .742
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30325808"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH-MGC 184"
/note="Organ: Pooled-glandular; Vector: pDNR-LIB; Site_1: SfiI (ggcattatggcc); Site_2: SfiI (ggcgctctggcc);

Library is oligo-dT primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATAGCC-3' and 3' adaptor sequence: 5'-ATTCAGAGCGCCGAGCAGATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 73.6%; Score 236.2; DB 6; Length 742;
Best Local Similarity 83.5%; Pred. No. 2,9e-63;
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTGCTTGTGGAGACAGAGTACC 60
93 GACATCCAGATGACCCAGTCTCCATCTCCCTGCTGCTTGTGGAGACAGAGTACC 152
61 ATCACTTGTGGACAAAGTCAAGCATTAAGCATTAATAATTGGTATCAGAGAAACA 120
153 ATCACTTGTGGACAAAGTCAAGCATTAAGCATTAATAATTGGTATCAGAGAAACA 212
121 GGACAGCCTCTAAGCTGCTCACTTACTGGGAGTCAACCCGGGAATCCGGGGTCCCTGAC 180
213 GGAAAAAGCCCCCTAAGCTGCTCACTTACTGGGAGTCAACCCGGGAATCCGGGGTCCCTGAC 272
181 CGATTCAGTGGAGCGGGTCTGGGACAGATTTCACTCTCAGCATCAGAGTCAACACT 240
273 AGGTTCAAGTGGAGCGGGTCTGGGACAGATTTCACTCTCAGCATCAGAGTCAACACT 332
241 GAAAGTTCTGCAACTTACTCTGTCAGCAGAGTTACAGATCCCGTACCTTTGGCCAG 300
333 GAAAGTTCTGCAACTTACTCTGTCAGCAGAGTTACAGATCCCGTACCTTTGGCCAG 392
301 GGGACCAAGCTGGAGATCAAA 321
393 GGGACCAAGCTGGAGATCAAA 413

RESULT 14 748 bp mRNA linear EST 29-APR-2003
CB956867
LOCUS AGENCOURT.13778741 NIH_MGC_184 Homo sapiens cDNA clone
DEFINITION IMAGE:30351770 5', mRNA sequence.

ACCESSION CB956867
VERSION CB956867.1 GI:30212984
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 748)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabp-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palokovits
cDNA Library Preparation: Clontech Laboratories, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNI at:
http://image.llnl.gov
Plate: NDCM149 row: n column: 03
High quality sequence stop: 528.

FEATURES

1..748 Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"

/db xref="taxon:9606"
/clone="IMAGE:30351770"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH_MGC_184"
/note="Organ: Pooled-glandular; Vector: pDNR-LIB; Site_1:
SfiI (ggccctcggcc); Site_2: SfiI (ggccctcggcc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATAGCC-3' and 3' adaptor sequence:
5'-ATTCAGAGCGCCGAGCAGATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 73.6%; Score 236.2; DB 6; Length 748;
Best Local Similarity 83.5%; Pred. No. 2,9e-63;
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTGCTTGTGGAGACAGAGTACC 60
93 GACATCCAGATGACCCAGTCTCCATCTCCCTGCTGCTTGTGGAGACAGAGTACC 154
61 ATCACTTGTGGACAAAGTCAAGCATTAAGCATTAATAATTGGTATCAGAGAAACA 120
155 ATCACTTGTGGACAAAGTCAAGCATTAAGCATTAATAATTGGTATCAGAGAAACA 214
121 GGACAGCCTCTAAGCTGCTCACTTACTGGGAGTCAACCCGGGAATCCGGGGTCCCTGAC 180
215 GGAAAAAGCCCCCTAAGCTGCTCACTTACTGGGAGTCAACCCGGGAATCCGGGGTCCCTGAC 274
181 CGATTCAGTGGAGCGGGTCTGGGACAGATTTCACTCTCAGCATCAGAGTCAACACT 240
275 AGGTTCAAGTGGAGCGGGTCTGGGACAGATTTCACTCTCAGCATCAGAGTCAACACT 334
241 GAAAGTTCTGCAACTTACTCTGTCAGCAGAGTTACAGATCCCGTACCTTTGGCCAG 300
335 GAAAGTTCTGCAACTTACTCTGTCAGCAGAGTTACAGATCCCGTACCTTTGGCCAG 394
301 GGGACCAAGCTGGAGATCAAA 321
395 GGGACCAAGCTGGAGATCAAA 415

RESULT 15 754 bp mRNA linear EST 01-MAY-2003
CB986767
LOCUS AGENCOURT.13647493 NIH_MGC_184 Homo sapiens cDNA clone
DEFINITION IMAGE:30329383 5', mRNA sequence.

ACCESSION CB986767
VERSION CB986767.1 GI:30281287
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 754)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabp-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palokovits
cDNA Library Preparation: Clontech Laboratories, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNI at:
http://image.llnl.gov

Plate: NDCM141 row: 1 column: 08
High quality sequence stop: 557.
Location/Qualifiers

FEATURES

Source

1..754

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGR:30329383"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH_MGC_184"

/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1: SfiI (ggccatattggcc); Site 2: SfiI (ggccgctcgcc); Library is oligo-dT primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC library."

ORIGIN

Query Match 73.6%; Score 236.2; DB 6; Length 754;
Best Local Similarity 83.5%; Pred. No. 2.9e-63;

Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY	1	GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTGCTGTGGAGACAGATCACC	60
DB	94	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTGCTGTGGAGACAGATCACC	153
QY	61	ATCCTTGTGGACAGATGACAGCATTAGCAGCTATTAAATTGGTATCAGCAAAACCA	120
DB	154	ATTACTTGGCGGGCAAGTCAAGACATTAGCAGCTATTAAATTGGTATCAGCAAAACCA	213
QY	121	GGAACAGCTCTTAAGTGTGCTCATTTACTGGCGATTACCCGGGAATCCGGGGTCCCTGAC	180
DB	214	GGGAATGCCCTTAAGTCTCTGATCTAATGTTGATCCAGTTTGCAAGTGGGGTCCCGACA	273
QY	181	CGATTGAGTGGCAGCGGGTCTGGGACAGATTTCATCTCACATCAGAGCTTACAACCT	240
DB	274	AGGTTGAGGGGAGTGGATCTGGGACAGCTTTCATCTCACATCAGAGCTTACAACCT	333
QY	241	GAAGATTCTGCAACTTACTACTGTACAGACAGATTACGACATCCCGTACACTTTTGGCCAG	300
DB	334	GAAGATTCTGCAACTTACTACTGTACAGACAGATTACGACATCCCGTACACTTTTGGCCAG	393
QY	301	GGGACCAAGCTGAGATCAAA	321
DB	394	GGGACCAAGCTGAGATCAAA	414

Search completed: December 7, 2004, 11:13:45
Job time : 1876.31 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 02:37:53 ; Search time 2155.18 Seconds
(without alignments)
8360.047 Million cell updates/sec

Title: US-09-403-107-143_COPY_1_381
Perfect score: 381
Sequence: 1 gaggtgcagctgcgtcgcagtc.....ccacggctcacgctccctca 381

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hlg: *
3: gb_in: *
4: gb_cm: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	379.4	99.6	381	6	AX003759	AX003759 Sequence
2	379.4	99.6	381	6	BD139667	BD139667 A novel m
3	379.4	99.6	414	6	A84376	A84376 Sequence 14
4	379.4	99.6	414	6	BD075294	BD075294 Novel met
5	378.4	99.3	1630	6	BD222939	BD222939 Heterom
6	378.4	99.3	1630	6	BD222939	BD222939 Heterom
7	378.4	99.3	1630	6	AX023365	AX023365 Sequence
8	378.4	99.3	1630	6	AX023367	AX023367 Sequence
9	351.2	92.2	438	9	HSR0127	HSR0127 H. sapiens r
10	336.8	88.4	378	9	HSR0127	HSR0127 H. sapiens r
11	336.8	88.4	378	9	HSR0127	HSR0127 H. sapiens r
12	330.8	86.7	381	9	AB021535	AB021535 Homo sapi
13	330.8	86.7	381	9	AB021535	AB021535 Homo sapi
14	325.4	85.4	384	9	HSR0127	HSR0127 H. sapiens r
15	324.8	85.2	360	9	AY607468	AY607468 Homo sapi
16	324.4	85.1	1413	6	BD185289	BD185289 Uses of a
17	324.4	85.1	1413	6	BD273725	BD273725 Human mon
18	324.4	85.1	1413	6	AR454402	AR454402 Sequence
19	324.4	85.1	1413	6	AX616568	AX616568 Sequence

20	324.2	85.1	391	9	AB021524	AB021524 Homo sapi
21	324	85.0	379	9	HSR0127	HSR0127 H. sapiens r
22	323.8	85.0	384	9	HSR0127	HSR0127 H. sapiens r
23	323.8	85.0	385	9	AB021508	AB021508 Homo sapi
24	323.2	84.8	429	6	E35220	E35220 Human monoc
25	322.2	84.6	381	9	AF174112	AF174112 Homo sapi
26	321.8	84.5	381	6	AX112590	AX112590 Sequence
27	321.6	84.4	369	9	AF062302	AF062302 Homo sapi
28	321.6	84.4	429	6	E35213	E35213 Human monoc
29	321.6	84.4	429	6	E35214	E35214 Human monoc
30	321.6	84.4	429	6	E35216	E35216 Human monoc
31	321.6	84.4	429	9	HSR0127	HSR0127 H. sapiens r
32	321.4	84.4	408	9	HSR0127	HSR0127 H. sapiens r
33	321.2	84.3	378	9	HSR0127	HSR0127 H. sapiens r
34	320.8	84.2	379	9	AB021507	AB021507 Homo sapi
35	320.8	84.2	762	12	SC0132609	SC0132609 Synthetic
36	320.4	84.1	435	9	AF431051	AF431051 Homo sapi
37	320.2	84.0	390	9	AB063901	AB063901 Homo sapi
38	320.2	84.0	424	12	AF453033	AF453033 Synthetic
39	319.6	83.9	368	9	HSR0127	HSR0127 H. sapiens r
40	319.6	83.9	375	9	HSR0127	HSR0127 H. sapiens r
41	319.4	83.8	378	9	AB063833	AB063833 Homo sapi
42	319.2	83.8	388	9	AF021971	AF021971 Homo sapi
43	318.4	83.6	384	12	AY315925	AY315925 Synthetic
44	318.4	83.6	429	6	E35212	E35212 Human monoc
45	317.8	83.4	396	9	HSR0127	HSR0127 H. sapiens r

ALIGNMENTS

RESULT 1	AX003759	381 bp	DNA	linear	PAT 24-AUG-2000
LOCUS	AX003759	Sequence 53 from Patent WO925818.			
DEFINITION	AX003759				
ACCESSION	AX003759				
VERSION	AX003759.1	GI:9927566			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Kufer, P. and Raum, T.				
AUTHORS					
TITLE	Method of identifying binding site domains that retain the capacity				
JOURNAL	Patent: WO 9925818-A 53 27-MAY-1999;				
FEATURES	KUFER PETER (DE); RAUM TOBIAS (DE)				
source	1. 381				
ORIGIN	/organism="Homo sapiens"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:9606"				
Query Match	99.6%; Score 379.4; DB 6; Length 381;				
Best Local Similarity	99.7%; Pred. No. 1.3e-108;				
Matches	380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	1 GAGGTGCACTGCTGCAAGTCTGGGGAGGCGCTGGTCCAGGAGGCTCCGAGACTC 60				
DB	1 GAGGTGCACTGCTGCAAGTCTGGGGAGGCGCTGGTCCAGGAGGCTCCGAGACTC 60				
QY	61 TCCTGTGACAGCCTGATTCACCTTCAGTAGCTATGATGACATGCGGTCGCCAGGCT 120				
DB	61 TCCTGTGACAGCCTGATTCACCTTCAGTAGCTATGATGACATGCGGTCGCCAGGCT 120				
QY	121 CCAGGCAAGGGGCTGAGTGGTGGCAGTTATATCATATGATGAGATTAATAATATCTAT 180				
DB	121 CCAGGCAAGGGGCTGAGTGGTGGCAGTTATATCATATGATGAGATTAATAATATCTAT 180				
QY	181 GCAGACTCCGTGTAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAAACAGCGTGTAT 240				
DB	181 GCAGACTCCGTGTAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAAACAGCGTGTAT 240				

Db	181	GCAGACTCCGTGAAAGAGGGCCGANTTACCACTTCGCAGAGCAACTTCGAAAGAACACCGCTGTAT	240		
Qy	241	CTGCAAATGAAACAGCCTTAGAGCTTAGAGACACAGCGCTGTGTATTACTGTGGCCGAAAGATATG	300		
Db	241	CTGCAAATGAAACAGCCTTAGAGCTTAGAGACACAGCGCTGTGTATTACTGTGGCCGAAAGATATG	300		
Qy	301	GGGTGGGGCAGTGGCTGTGAGACCCCTACTACTACTACGATATATGACGCTGTGGGGCCCAAGG	360		
Db	301	GGGTGGGGCAGTGGCTGTGAGACCCCTACTACTACTACGATATATGACGCTGTGGGGCCCAAGG	360		
Qy	361	ACCAAGCTTCACCGTCTCTCTCA	381		
Db	361	ACCAAGCTTCACCGTCTCTCTCA	381		
RESULT 2	BD139667	381 bp	DNA	linear	PAT 18-SEP-2002
LOCUS	BD139667				
DEFINITION	A novel method of identifying binding site domains that retain the capacity of binding to an epitope.				
ACCESSION	BD139667				
VERSION	BD139667.1	GI:23234612			
KEYWORDS	JP 2002508924-A/52.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eumetazoa; Euteleostomi; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Kufner,P., Raun,T., Borschert,K., Zetzl,F. and Lutterbuese,R.				
TITLE	A novel method of identifying binding site domains that retain the capacity of binding to an epitope				
JOURNAL	Patent: JP 2002508924-A 52 26-MAR-2002;				

	COMMENT
OS	Homo sapiens (human)
PN	JP 2002508924-A/52
PD	26-MAR-2002
PF	16-NOV-1998 JP 2000521184
PR	17-NOV-1997 EP 97120096.9
PI	PETER KUJBER, TOBIAS RAMM, KATRIN BORSCHERT, FLORIAN ZETTL, RALF LUTTERBUSE
PC	C12N15/09,A6IK38/00,A6IK38/22,A6IK39/395,C07K14/705,
PC	C07K16/30,
PC	C12N1/21,C12N5/10,C12P21/02,C12P21/08,G01N33/566,C12N15/00, PC A6IK37/02,
PC	A6IK37/24,A6IK37/48,C12N5/00
CC	A novel method of identifying binding site domains that retain the capacity of binding to an epitope key
CC	the
CC	capacity of binding to an epitope
FH	Location/Qualifiers
FT	source
FT	1..381
FT	/Organism='Homo sapiens (human)'. Location/Qualifiers
FEATURES	1..381
source	/Organism="Homo sapiens"
	/mol_type="genomic DNA"
	/db_xref="taxon:9606"
ORIGIN	

Query Match	99.6%	Score 379.4	DB 6	Length 381
Best Local Similarity	99.7%	Pred. No. 1.3e-108		
Matches 380	Conservative 0	Mismatches 1	Indels 0	Gaps 0
QY	1	GAGGTGACAGTCTCGAGTCTGGGGAGGCGCTGTCACAGCTGGAGAGTCCCTGAGACTC	60	
Db	1	GAGGTGACAGTCTCGAGTCTGGGGAGGCGGTGTCACAGCTGGAGAGTCCCTGAGACTC	60	
QY		TCCTGTGACGCGCTCTGGAGATTCACTTCACTAGTATGGATGACATGGGTCCGCGAGGCT	120	
Db	61	TCCTGTGACGCGCTCTGGAGATTCACTTCACTAGTATGGAGATGACATGGGTCCGCGAGGCT	120	
QY	121	CCAGGCAAGGGCTGAGTGGGTGGCAGTTAATCATATGATGAGATATAAATCTAT	180	

Db	121	CCAGGCAAGGGGGCTGAGATGGGTGGCAATTATATCATATGATGGAAGTAATAAATACTAT	180
QY	181	GCAGACTTCCTGGAAAGGGCCGATTTCCACCTCTTCAGAGACAAATTCCAAGAACGCTGTAT	240
Db	181	GCAGACTTCCTGGAAAGGGCCGATTTCCACCTCTTCAGAGACAAATTCCAAGAACGCTGTAT	240
QY	241	CTGCMAATGAACAAGCCTGAGAGCTGAGAGACAAGCGCTGTATTACTGTGCGAAAGATATG	300
Db	241	CTGCMAATGAACAAGCCTGAGAGCTGAGAGACAAGCGCTGTATTACTGTGCGAAAGATATG	300
QY	301	GGGTGGGGCAATGAGCTGGAGACCCCTACTACTATCTACGGATATGACGCTCTGGGGCCAAAGG	360
Db	301	GGGTGGGGCAATGAGCTGGAGACCCCTACTACTACTACGGATATGACGCTCTGGGGCCAAAGG	360
QY	361	ACCAAGGTCAACGCTCCTCA	381
Db	361	ACCAAGGTCAACGCTCCTCA	381

RESULT 3			
LOCUS	A84376	414 bp	DNA
DEFINITION	Sequence 143 from Patent WO946645.		
ACCESSION	A84376		
VERSION	A84376.1	GI:6733299	
KEYWORDS	.		
SOURCE	unidentified		
ORGANISM	unidentified		
REFERENCE	unclassified.		
AUTHORS	1 (bases 1 to 414)		
TITLE	Kiefer P. and Raum T.		
JOURNAL	NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN RECEPTORS AND USES THEREOF		
FEATURES	Patent: WO 9846645-A 143 22-OCT-1998;		
source	KUEFER PETER (DE); RAUM TOBIAS (DE)		
	Location/Qualifiers		
	1..414		

```

CDS
        /mol_type="unassigned DNA"
        /db_xref="taxon:32644"
        <1..>414
        /note="unnamed protein product"
        /codon_start=1
        /protein_id="CAB69288.1"
        /db_xref="GI:6733300"
        /translation="EVQLLESGGSGVQPGFSLRLSCAASGFTSSVGMHWVRQAPGKG
LEMAVATISYDGSNKTADSVKGRFTISRDNSKTKLTIQNMSLRAEDTAVYYCAQDMGM
GSGGRPYYYGMDVMVGSGTIVTIVSSAPTKAPPEPL"

```

ORIGIN	Query Match	99.6%;	Score 379.4;	DB 6;	Length 414;
	Best Local Similarity	99.7%;	Pred. No. 1.4e-108;		
	Matches 380;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0
QY	1	GAGGTGCAGCTGTCTGAGTCTTGGGGGAGGCCCTTGCCAGCCTCGGGAGAGTCCCTGAGACTTC	60		
Db	1	GAGGTGCAGCTGTCTGAGTCTTGGGGGAGGCCCTTGCCAGCCTCGGGAGAGTCCCTGAGACTTC	60		
QY	61	TCCTGTGAGGCTCTGGAATTCACCTTCAGTAGCTATGAGATGCACTGGGGTCCGCAGAGCT	120		
Db	61	TCCTGTGAGGCTCTGGAATTCACCTTCAGTAGCTATGAGATGCACTGGGGTCCGCAGAGCT	120		
QY	121	CCAGGCAAGGGGGCTGAGTGGGTGGCAATTTATCATATGATGGAAGTAATTAATCTAT	180		
Db	121	CCAGGCAAGGGGGCTGAGTGGGTGGCAATTTATCATATGATGGAAGTAATTAATCTAT	180		
QY	181	GCAGACTCCGTGAAGGGGCCGATTCAACCATCTCCAGAGACAAATTCCAAGAAACGCGTGTAT	240		
Db	181	GCAGACTCCGTGAAGGGGCCGATTCAACCATCTCCAGAGACAAATTCCAAGAAACGCGTGTAT	240		
QY	241	CTGCAGATGAACAAGCTGAGAGCTGAGGACACGCGCTGTGTATTACTGTGCGAAAGATATAG	300		
Db	241	CTGCAGATGAACAAGCTGAGAGCTGAGGACACGCGCTGTGTATTACTGTGCGAAAGATATAG	300		

QY 301 GGGTGGGGGAGTGGCTGGAGACCCCTACTACTACTAGGATATGAGCGTCTGGGGCCAAAGG 360
DB 301 GGGTGGGGGAGTGGCTGGAGACCCCTACTACTACTAGGATATGAGCGTCTGGGGCCAAAGG 360
QY 361 ACCACGGTACCGTCTCTCA 381
DB 361 ACCACGGTACCGTCTCTCA 381

RESULT 4
LOCUS BD075294 414 bp DNA linear PAT 27-AUG-2002
DEFINITION Novel method for the production of anti-human antigen receptors and uses thereof.
ACCESSION BD075294
VERSION BD075294.1 GI:22620897
KEYWORDS JP 2001519824-A/23.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 414)
AUTHORS Kufer,P. and Raum,T.
TITLE Novel method for the production of anti-human antigen receptors and uses thereof
JOURNAL Patent: JP 2001519824-A 23 23-OCT-2001;
MICROMET AG
COMMENT OS Homo sapiens (human)
PN JP 2001519824-A/23
PD 23-OCT-2001
PF 14-APR-1998 JP 1998543494
PR 14-APR-1997 EP 97106109.8
PI PETER KUFER, TOBIAS RAUM
PC C07K16/00,C07K16/30,A61K39/395
CC Novel method for the production of anti-human antigen CC
receptors and uses
CC thereof
FH Key
FT CDS Location/Qualifiers
source 1..414
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 99.6%; Score 379.4; DB 6; Length 414;
Best Local Similarity 99.7%; Pred. No. 1.4e-108;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGGTGACAGTGTCTGAGTCTGGGGGAGGCGCTGATCCAGCTGGAGTCCCTGAGACTC 60
DB 1 GAGGTGACAGTGTCTGAGTCTGGGGGAGGCGCTGATCCAGCTGGAGTCCCTGAGACTC 60
QY 61 TCTGTGACAGCTCTGATTCACCTTCAGTACCTAGTGGAGTGGAGTCCGCGCAGGCT 120
DB 61 TCTGTGACAGCTCTGATTCACCTTCAGTACCTAGTGGAGTGGAGTCCGCGCAGGCT 120
QY 121 CCAGGCAAGGGGGGTGAGTGGGGGAGGATATATCATATGATGAGAGTAAATATCTAT 180
DB 121 CCAGGCAAGGGGGGTGAGTGGGGGAGGATATATCATATGATGAGAGTAAATATCTAT 180
QY 181 GCAGACTCCGTGAGAGGGCCGATTCAACATCTCCAGAGACAATTCAGAGACGCTGTAT 240
DB 181 GCAGACTCCGTGAGAGGGCCGATTCAACATCTCCAGAGACAATTCAGAGACGCTGTAT 240
QY 241 CTGCAATGAACAGCTTGAGAGCTGAGAGACAGCGCTGTATTAATTAATTAATGATG 300
DB 241 CTGCAATGAACAGCTTGAGAGCTGAGAGACAGCGCTGTATTAATTAATTAATGATG 300
QY 301 GGGTGGGGGAGTGGCTGGAGACCCCTACTACTACTAGGATATGAGCGTCTGGGGCCAAAGG 360

DB 301 GGGTGGGGGAGTGGCTGGAGACCCCTACTACTACTAGGATATGAGCGTCTGGGGCCAAAGG 360
QY 361 ACCACGGTACCGTCTCTCA 381
DB 361 ACCACGGTACCGTCTCTCA 381

RESULT 5
LOCUS BD222938 1630 bp DNA linear PAT 17-JUL-2003
DEFINITION Heteromindodies.
ACCESSION BD222938
VERSION BD222938.1 GI:33032708
KEYWORDS UP 2002521053-A/32.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1630)
AUTHORS Kufer,P., Dreier,T., Baerle,P.A., Borschert,K. and Zettl,F.
TITLE Heteromindodies
JOURNAL Patent: JP 2002521053-A 32 16-JUL-2002;
MICROMET AG
COMMENT OS Homo sapiens (human)
PN Mus musculus (mouse)
PD 16-JUL-2002
PF 28-JUL-1999 JP 2000562401
PR 28-JUL-1998 EP 98114082.5
PI PETER KUFER, TORSTEN DREIER, PATRICK A BAERLE, KATRIN BORSCHERT
PI FLORIAN ZETTL
PC C12N15/09,A61K35/76,A61K38/00,A61K38/21,A61P35/00,A61P35/02,
PC C07K19/00,
PC C12N5/10,C12P21/02,G01N33/53,G01N33/53// (C12N5/10,C12R1.91),
PC (C12P21/02,C12R1.91), C12N15/00,C12N5/00,A61K37/02,A61K37/66,
PC (C12N5/00,C12R1.91)
CC Heteromindodies
CC Heteromindodies
FH Key
FT CDS Location/Qualifiers
source 1..1630
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 99.3%; Score 378.4; DB 6; Length 1630;
Best Local Similarity 99.7%; Pred. No. 3.3e-108;
Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGGTGACAGTGTCTGAGTCTGGGGGAGGCGCTGATCCAGCTGGAGTCCCTGAGACTC 60
DB 462 GAGGTGACAGTGTCTGAGTCTGGGGGAGGCGCTGATCCAGCTGGAGTCCCTGAGACTC 521
QY 61 TCTGTGACAGCTCTGATTCACCTTCAGTACCTAGTGGAGTGGAGTCCGCGCAGGCT 120
DB 522 TCTGTGACAGCTCTGATTCACCTTCAGTACCTAGTGGAGTGGAGTCCGCGCAGGCT 120
QY 121 CCAGGCAAGGGGGGTGAGTGGGGGAGGATATATCATATGATGAGAGTAAATATCTAT 180
DB 121 CCAGGCAAGGGGGGTGAGTGGGGGAGGATATATCATATGATGAGAGTAAATATCTAT 180
QY 582 CCAGGCAAGGGGGGTGAGTGGGGGAGGATATATCATATGATGAGAGTAAATATCTAT 641
DB 582 CCAGGCAAGGGGGGTGAGTGGGGGAGGATATATCATATGATGAGAGTAAATATCTAT 641
QY 181 GCAGACTCCGTGAGAGGGCCGATTCAACATCTCCAGAGACAATTCAGAGACGCTGTAT 240
DB 642 GCAGACTCCGTGAGAGGGCCGATTCAACATCTCCAGAGACAATTCAGAGACGCTGTAT 240
QY 241 CTGCAATGAACAGCTTGAGAGCTGAGAGACAGCGCTGTATTAATTAATTAATGATG 300
DB 702 CTGCAATGAACAGCTTGAGAGCTGAGAGACAGCGCTGTATTAATTAATTAATGATG 300
QY 301 GGGTGGGGGAGTGGCTGGAGACCCCTACTACTACTAGGATATGAGCGTCTGGGGCCAAAGG 360

Db 762 GGGTGGGGGAGTGGCTGAGAGACCCCTACTACTAGGTATGAGCTGTGGGCCAAGGG 821

QY 361 ACCACGGTCAACCGTCTCTC 380

Db 822 ACCACGGTCAACCGTCTCTC 841

RESULT 6
BD222939
LOCUS BD222939 1630 bp DNA linear PAT 17-JUL-2003
DEFINITION Heteromnibodies.
ACCESSION BD222939
VERSION BD222939.1 GI:33032709
KEYWORDS JP 2002521053-A/33.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1630)
AUTHORS Kufer,P., Dreier,T., Baeuerle,P.A., Borschert,K. and Zetl,F.
TITLE Heteromnibodies
JOURNAL Patent: JP 2002521053-A 33 16-JUL-2002;
MICROMET AG

COMMENT OS Homo sapiens (human)
OS Mus musculus (mouse)
PN JP 2002521053-A/33
PD 16-JUL-2002 JP 2000562401
PF 28-JUL-1999 JP 2000562401
PR 28-JUL-1998 EP 98114082.5
PI PETER KUFER, TORSTEN DREIER, PATRICK A BAEUERLE, KATRIN BORSCHERT,
BORSCHERT,
PI FLORIAN ZETTL
PC C12N15/09,A61K35/76,A61K38/00,A61K38/21,A61P35/00,A61P35/02,
PC C07K19/00,
PC C12N5/10,C12P21/02,G01N33/53,G01N33/53// (C12N5/10,C12R1.91),
PC (C12P21/02,C12R1.91),C12N15/00,C12N5/00,A61K37/02,A61K37/66,
PC (C12N5/00,C12R1.91)
CC Heteromnibodies
FH Key
FT CDS Location/Qualifiers
1..1630
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 99.3%; Score 378.4; DB 6; Length 1630;
Best Local Similarity 99.7%; Pred. No. 3.3e-108;
Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGGTGACAGCTGTCGAGTCTGGGGAGGCGCTGTCACGCTGGAGGTCCTTGAGACTC 60
Db 462 GAGGTGACAGCTGTCGAGTCTGGGGAGGCGCTGTCACGCTGGAGGTCCTTGAGACTC 521

QY 61 TCCTGAGAGCTCTGAGATTCACTTCAGTAGCTATGAGTACCTGGGTCGCGCAGGCT 120
Db 522 TCCTGAGAGCTCTGAGATTCACTTCAGTAGCTATGAGTACCTGGGTCGCGCAGGCT 581

QY 121 CCAGGCAAGGGGCTGAGTGGGTGGAGTTATATCATATGATGAGATTAATACTAT 180
Db 582 CCAGGCAAGGGGCTGAGTGGGTGGAGTTATATCATATGATGAGATTAATACTAT 641

QY 181 GCAAGATCCGTGAAGGGCCGATTCAACATCTCCAGAGACAATTCACAAGAACGCTGTAT 240
Db 642 GCAAGATCCGTGAAGGGCCGATTCAACATCTCCAGAGACAATTCACAAGAACGCTGTAT 701

QY 241 CTGCAAAATGAACAGCTGAGCTGAGAGCAAGGCTGTATTAATCTGCGAAAGATATG 300
Db 702 CTGCAAAATGAACAGCTGAGCTGAGAGCAAGGCTGTATTAATCTGCGAAAGATATG 761

QY 301 GGGTGGGGGAGTGGCTGAGAGACCTTACTACTACGATATGAGCTGTGGGCCCAAGGG 360

Db 762 GGGTGGGGGAGTGGCTGAGAGACCCCTACTACTAGGTATGAGCTGTGGGCCAAGGG 821

QY 361 ACCACGGTCAACCGTCTCTC 380

Db 822 ACCACGGTCAACCGTCTCTC 841

RESULT 7
AX023365
LOCUS AX023365 1630 bp DNA linear PAT 15-SEP-2000
DEFINITION Sequence 36 from Patent WO0006605.
ACCESSION AX023365
VERSION AX023365.1 GI:10183777
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Kufer,P., Zetl,F., Dreier,T., Baeuerle,P.A. and Borschert,K.
TITLE Heteromnibodies
JOURNAL Patent: WO 0006605-A 36 10-FEB-2000;
KUFER PETER (DE) ; ZETTL FLORIAN (DE) ;
BAEUEERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GBS FUER BIOMEDIZINIS (DE)

FEATURES
source
1..1630
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
39..1610
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC08835.1"
/db_xref="GI:10183778"
/translation="MGMSCKILFLVATATGVNHSLOMTQSPSSLSASVGDRTVTCRA
SOSISYLNWYQKGPPLKIYVASFRESGVPDRFSGSSGTATLTLSLOPEDF
ATVPCQSDSLPIPTFGGCTRLDIOGGGGGGGGGGSGSEVQLLESGGGVQPSLR
LSCASGTFSSYGMHWRAQPKGLBENVAVISYDGSKRYVADSYKGFTRSDSKN
TLVLDWNSLRLABDVAIVYICADMGWGSGRPIYYGMVWQGTIVTVSSGTPLEDIT
HTASTKGPSPFLAPSSKSTSGDTALDCLVKDYRPEPTVSWNSGALTSVHTPPAV
LQSSGLYSLSVTVVPSLSLGTQYICVNHKPSNTKVDKVEPSGCDTSGGSGSAP
ARSPSPSTQPEWHVVAIOEARLLNLSDTAENMEVTEVISEMFDLOBPTCLQRLR
LYKQGLRSLIKTKGKLPLTMASHVYQHCPPTPEISCAIQIITFESFKENLQDFLLVIP
FDCHRPVDEHHHHH"

ORIGIN

Query Match 99.3%; Score 378.4; DB 6; Length 1630;
Best Local Similarity 99.7%; Pred. No. 3.3e-108;
Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGGTGACAGCTGTCGAGTCTGGGGAGGCGCTGTCACGCTGGAGGTCCTTGAGACTC 60
Db 462 GAGGTGACAGCTGTCGAGTCTGGGGAGGCGCTGTCACGCTGGAGGTCCTTGAGACTC 521

QY 61 TCCTGAGAGCTCTGAGATTCACTTCAGTAGCTATGAGTACCTGGGTCGCGCAGGCT 120
Db 522 TCCTGAGAGCTCTGAGATTCACTTCAGTAGCTATGAGTACCTGGGTCGCGCAGGCT 581

QY 121 CCAGGCAAGGGGCTGAGTGGGTGGAGTTATATCATATGATGAGATTAATACTAT 180
Db 582 CCAGGCAAGGGGCTGAGTGGGTGGAGTTATATCATATGATGAGATTAATACTAT 641

QY 181 GCAAGATCCGTGAAGGGCCGATTCAACATCTCCAGAGACAATTCACAAGAACGCTGTAT 240
Db 642 GCAAGATCCGTGAAGGGCCGATTCAACATCTCCAGAGACAATTCACAAGAACGCTGTAT 701

QY 241 CTGCAAAATGAACAGCTGAGCTGAGAGCAAGGCTGTATTAATCTGCGAAAGATATG 300
Db 702 CTGCAAAATGAACAGCTGAGCTGAGAGCAAGGCTGTATTAATCTGCGAAAGATATG 761

QY 301 GGGTGGGGGAGTGGCTGAGAGACCTTACTACTACGATATGAGCTGTGGGCCCAAGGG 360

Db 762 GGGTGGGAGTGGCTGAGACCCCTACTACTACGATGAGCGTCTGGGGCCAAGG 821
QY 361 ACCAGGTCACCGTCTCTC 380
Db 822 ACCAGGTCACCGTCTCTC 841

RESULT 8
AX023367
LOCUS AX023367 1630 bp DNA linear PAT 15-SEP-2000
DEFINITION Sequence 38 from Patent WO0006605.
ACCESSION AX023367
VERSION AX023367.1 GI:10183779
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1
TITLE Kufer, P., Zetli, F., Dreier, T., Baerle, P.A. and Borschert, K.
JOURNAL Heteromindodies
Patent: WO 0006605-A 38 10-FEB-2000;
KUFER PETER (DE) ; ZETTL FLORIAN (DE) ; DREIER TORSTEN (DE) ;
BAERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GBS FUER
BIOMEDIZINIS (DE)
FEATURES
source 1.1630
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
39..1613
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC08836.1"
/db_xref="GI:10183780"

CDS
/translation="MGMSCTILFLVATGVHSELOMTQSPSSLSASVDRTITCRA
/translacion="MGMSCTILFLVATGVHSELOMTQSPSSLSASVDRTITCRA
SOSISYLNMYOQKPGQPKLIVMASTRSGVDPBPSGSEGTNTYLLTISLQEPD
ATYPCQSDSLPTFGQRLDIOGGGGGGGGGGSEVOLLESGGVODGRSLR
LSCAGSGTPSSGYGMHVRQARBKLEMAVVISYDSNRYADSVKGRITISDNKN
TLYLQMSRLRAEDTAVYCAKMGWSGMRPIYTGMDWGOCTVTVSSGFLGDT
HRTVAAPSVFIFPPSEDKSGTASVCLNNFYPRKRVOMKDNALQSGGOSV
TEODSKSTYSLSTLTLSKADYERKIVACEVTHQGLSPVSKFNRGSCGGGSA
PTSSKTKTOLQLEHLLDLOMLINGINNYKNPKLRMLTFKRYMKKATLKHLCCL
EEELKLEEVLLAOSKNFHLRPDISININIVLELKSEFTTFMEVADETATIEF
LNRMTFCOSIISTLT"

ORIGIN
Query Match 99.3%; Score 378.4; DB 6; Length 1630;
Best Local Similarity 99.7%; Pred. No. 3.3e-108;
Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 GAGGTGCACTGCTGAGTCTGGGGGAGGCTGCTCAGCTGGAGGTCCTGAGACTC 60
Db 462 GAGGTGCACTGCTGAGTCTGGGGGAGGCTGCTCAGCTGGAGGTCCTGAGACTC 521
QY 61 TCTGTGCAAGCCTCTGATTCACCTTCAGTAGTATGCGACTGGGTCGCCAGGCT 120
Db 522 TCTGTGCAAGCCTCTGATTCACCTTCAGTAGTATGCGACTGGGTCGCCAGGCT 581
QY 121 CCAGGCAAGGGGCTGAGTGGTGGAGTTATATCATATGATGAGTAAATACTAT 180
Db 582 CCAGGCAAGGGGCTGAGTGGTGGAGTTATATCATATGATGAGTAAATACTAT 641
QY 181 GCAAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACAGCTGTAT 240
Db 642 GCAAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACAGCTGTAT 701
QY 241 CTGCAATGAACAGCTGAGAGTGAAGACACGGCTGTATTAATCTGCGAAAGTATG 300
Db 702 CTGCAATGAACAGCTGAGAGTGAAGACACGGCTGTATTAATCTGCGAAAGTATG 761
QY 301 GGGTGGGAGTGGCTGAGACCCCTACTACTACGATGAGCGTCTGGGGCCAAGG 360

Db 762 GGGTGGGAGTGGCTGAGACCCCTACTACTACGATGAGCGTCTGGGGCCAAGG 821
QY 361 ACCAGGTCACCGTCTCTC 380
Db 822 ACCAGGTCACCGTCTCTC 841

RESULT 9
HSR0127
LOCUS HSR0127 438 bp mRNA linear PRI 29-FEB-1996
DEFINITION H.sapiens rearranged VDU region (R0U127).
ACCESSION X81745
VERSION X81745.1 GI:1212972
KEYWORDS diverse region; immunoglobulin heavy chain; joining region;
variable region; VH-3 family.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1
TITLE Mili, M., Schiff, C., Fougereau, M. and Tonnelle, C.
JOURNAL The VDU repertoire expressed in human pres cells reflects the
selection of bona fide heavy chains
Eur. J. Immunol. 26 (1), 63-69 (1996)
MEDLINE 96152725
PubMed 8566085
REFERENCE 2 (bases 1 to 438)
AUTHORS Tonnelle, C.
TITLE Direct Submision
JOURNAL Submitted (15-SEP-1994) C. Tonnelle, Centre d'Immunologie
Marseille-Luminy, Case 906, 13288 Marseille, Cedex 9, FRANCE
COMMENT Related sequences: X65741, X65883 to X65920.
FEATURES
source 1.438
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="14"
/clone="R0U 127"
/cell_type="pre B-lymphocytes"
/tissue_type="bone marrow"
/clone_1ib="R0U"
/rearranged
1..57
sig_peptide 58..353
V_region
/product="immunoglobulin heavy chain V region"
D_segment 354..376
/product="immunoglobulin heavy chain D segment"
J_segment 377..438
/product="immunoglobulin heavy chain J segment"

ORIGIN
Query Match 92.2%; Score 351.2; DB 9; Length 438;
Best Local Similarity 95.3%; Pred. No. 1.1e-99;
Matches 362; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

2 AGGTGCACTGCTGAGTCTGGGGGAGGCTGCTCAGCTGGAGGTCCTGAGACTC 61
Db 59 AGGTGCACTGCTGAGTCTGGGGGAGGCTGCTCAGCTGGAGGTCCTGAGACTC 118
QY 62 CCTGTGCAAGCCTCTGATTCACCTTCAGTAGTATGCGACTGGGTCGCCAGGCT 121
Db 119 CCTGTGCAAGCCTCTGATTCACCTTCAGTAGTATGCGACTGGGTCGCCAGGCT 178
QY 122 CAGGCAAGGGGCTGAGTGGTGGAGTTATATCATATGATGAGTAAATACTATG 181
Db 179 CAGGCAAGGGGCTGAGTGGTGGAGTTATATCATATGATGAGTAAATACTATG 238
QY 182 CAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACAGCTGTAT 241
Db 239 CAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACAGCTGTAT 298
QY 242 TCGCAATGAACAGCTGAGAGTGAAGACACGGCTGTATTAATCTGCGAAAGTATG 301

Db 299 TGAATGAAACACCTGAGAGCTGAGACACGCTGTGTATTACTGTGGAAGAAAGG 358
QY 302 GGTGGGGCAGTGGCTGAGACCTCTACTACTACCGATGACGCTCTGGGGCAGAGGA 361
Db 359 GGGGGTTCCTCCCGCGGACATTACTACTACTAGAGTATGACGCTCTGGGGCAGAGGA 418
QY 362 CCACGGTCAACGCTCTCTCA 381
Db 419 CCACGGTCAACGCTCTCTCA 438
RESULT 10
HSA579147 378 bp mRNA linear PRI 01-JUN-2004
LOCUS HSA579147
DEFINITION Homo sapiens partial mRNA for Igm immunoglobulin heavy chain
ACCESSION AJ579147
VERSION AJ579147.1 GI:47846472
KEYWORDS IGHV3-30 gene; immunoglobulin heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Dono, M.
TITLE Characterization of a novel CD5+ B cell population
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 378)
AUTHORS Dono, M.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2003) Dono M., Oncologia Medica C., Istituto Nazionale Ricerca sul Cancro, L. go R. Benzi 10, Genova, 16132, ITALY
FEATURES
source Location/Qualifiers
1..378
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="14"
/clone="T2.3.9"
/tissue_type="tonsil"
/rearranged
/country="Italy:Genova"
1..378
/gene="IGHV3-30"
/db_xref="GI:47846473"
/protein_id="CAE45401.1"
/product="immunoglobulin heavy chain variable region"
/translation="QVQLVSGGAVQPGRIQLSCASGFTFSYGMHWVROAPGK
LEWVAIVSYDGSNRYADSVKGRFTISRNISKNTLYLQMSLRADPTAVYCAKQGY
YDGKYYYYGMDVWGQGTITVYS"
<1..>378
/gene="IGHV3-30"
/product="immunoglobulin heavy chain variable region"
ORIGIN
Query Match 88.4%; Score 336.8; DB 9; Length 378;
Best Local Similarity 94.7%; Pred. No. 4e-95; Indels 3; Gaps 1;
Matches 360; Conservative 0; Mismatches 17;
Db 2 AGGTGAGCTGTGAGTCTGGGGAGGCGCTGCTCCAGCTGGAGTCCCTGAGACTCT 61
QY 2 AGGTGAGCTGTGAGTCTGGGGAGGCGCTGCTCCAGCTGGAGTCCCTGAGACTCT 61
Db 2 AGGTGAGCTGTGAGTCTGGGGAGGCGCTGCTCCAGCTGGAGTCCCTGAGACTCT 61
QY 62 CCTGTGACAGCTTGTGATTCACCTTCAAGTACGATGACGCTGGTCCGCGAGGCTTC 121
Db 62 CCTGTGACAGCTTGTGATTCACCTTCAAGTACGATGACGCTGGTCCGCGAGGCTTC 121
QY 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGTAATAATACTATG 181

Db 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGTAATAATACTATG 181
QY 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGACAAATTCAGAAACAGCTGTATC 241
Db 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGACAAATTCAGAAACAGCTGTATC 241
QY 242 TGCATATGAACAGCTTGAAGAGTGAAGACAGGCTGTGTATTAATCTGTGCGAAAGTATAG 301
Db 242 TGCATATGAACAGCTTGAAGAGTGAAGACAGGCTGTGTATTAATCTGTGCGAAAGTATAG 301
QY 302 GGTGGGGCAGTGGCTGAGACCTCTACTACTACGATGACGCTGGGGCAGAGGA 361
Db 299 AGTATTACTATGATGGAATATCTACTACTACGATGACGCTCTGGGGCAGAGGA 358
QY 362 CCACGGTCAACGCTCTCTCA 381
Db 359 CCACGGTCAACGCTCTCTCA 378
RESULT 11
HSA579148 378 bp mRNA linear PRI 01-JUN-2004
LOCUS HSA579148
DEFINITION Homo sapiens partial mRNA for Igm immunoglobulin heavy chain
ACCESSION AJ579148
VERSION AJ579148.1 GI:47846474
KEYWORDS IGHV3-30 gene; immunoglobulin heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Dono, M.
TITLE Characterization of a novel CD5+ B cell population
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 378)
AUTHORS Dono, M.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2003) Dono M., Oncologia Medica C., Istituto Nazionale Ricerca sul Cancro, L. go R. Benzi 10, Genova, 16132, ITALY
FEATURES
source Location/Qualifiers
1..378
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="14"
/clone="T2.3.10"
/tissue_type="tonsil"
/rearranged
/country="Italy:Genova"
1..378
/gene="IGHV3-30"
/db_xref="GI:47846475"
/protein_id="CAE45402.1"
/product="immunoglobulin heavy chain variable region"
/translation="QVQLVSGGAVQPGRIQLSCASGFTFSYGMHWVROAPGK
LEWVAIVSYDGSNRYADSVKGRFTISRNISKNTLYLQMSLRADPTAVYCAKQGY
YDGKYYYYGMDVWGQGTITVYS"
<1..>378
/gene="IGHV3-30"
/product="immunoglobulin heavy chain variable region"
ORIGIN
Query Match 88.4%; Score 336.8; DB 9; Length 378;
Best Local Similarity 94.7%; Pred. No. 4e-95; Indels 3; Gaps 1;
Matches 360; Conservative 0; Mismatches 17;
QY 2 AGGTGAGCTGTGAGTCTGGGGAGGCGCTGCTCCAGCTGGAGTCCCTGAGACTCT 61

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 22:52:33 ; Search time 322.553 Seconds
 (without alignments)
 6200.629 Million cell updates/sec

Title: US-09-403-107-143_COPY_1_381
 Perfect score: 381
 Sequence: 1 gaggtgcagctgcgtcgagtc.....ccacggcaccgtctcctca 381

Scoring table: IDENTITY NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
 1: geneseqn1808:*
 2: geneseqn1908:*
 3: geneseqn2008:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	379.4	99.6	381	2	AAx77236	Aax77236 Human DA.
2	379.4	99.6	414	2	AAV68537	Aav68537 Nucleotid
3	378.4	99.3	1630	2	AAZ50588	Aaz50588 HD70scFv-
4	378.4	99.3	1630	3	AAZ50587	Aaz50587 HD70scFv-
5	324.4	85.1	1413	3	AAA46898	Aaa46898 DNA encod
6	324.4	85.1	1413	10	AAZ54349	Aaz54349 Human 11.
7	324.4	85.0	378	12	ADP22221	Adp22221 Human ant
8	324.4	85.0	382	10	ADK18651	Adk18651 Anti-huma
9	324.4	85.0	382	12	ADL25435	Adl25435 Human mab
10	323.2	84.8	372	12	ADP22135	Adp22135 Human ant
11	323.2	84.8	429	3	AAA13939	Aaa13939 Human PTH
12	322.8	84.7	375	12	ADP22315	Adp22315 Human ant
13	322.4	84.6	379	10	ADL25419	Adl25419 Human mab
14	322.4	84.6	379	12	ADL25419	Adl25419 Human mab
15	321.8	84.5	381	4	AAV68537	Aav68537 DNA encod
16	321.6	84.4	429	3	AAA13933	Aaa13933 Human PTH
17	321.6	84.4	429	3	AAA13935	Aaa13935 Human PTH
18	321.6	84.4	429	3	AAA13932	Aaa13932 Human PTH
19	321.2	84.3	375	12	ADP22289	Adp22289 Human ant
20	321.2	84.3	375	12	ADP22311	Adp22311 Human ant
21	320.8	84.2	379	10	ADK18655	Adk18655 Anti-huma

22	320.8	84.2	379	12	ADL25403	Adl25403 Human mab
23	320.6	84.1	384	12	ADP22159	Adp22159 Human ant
24	320.4	84.1	474	8	ABZ22308	Abz22308 S. pneumo
25	318.4	83.6	429	3	AAA13931	Aaa13931 Human PTH
26	318.4	83.5	375	12	ADP22167	Adp22167 Human ant
27	318.4	83.5	375	12	ADP22099	Adp22099 Human ant
28	318.4	83.5	437	6	ABL53511	AbL53511 Human rec
29	318.4	83.5	437	6	ABL53512	AbL53512 Human rec
30	318.4	83.5	487	8	AAV68537	Aav68537 Human AB-
31	318.4	83.5	7576	8	AAV68537	Aav68537 Human AB-
32	317.6	83.4	366	12	ADP22127	Adp22127 Human ant
33	317.6	83.4	372	9	ADP22127	Adp22127 Human ant
34	316.8	83.1	373	10	ADL28438	AdL28438 Human ant
35	316.8	83.1	429	3	AAA13936	Aaa13936 Human PTH
36	316.4	83.0	375	12	ADP22331	Adp22331 Human ant
37	316.4	83.0	375	12	ADP22163	Adp22163 Human ant
38	316.4	83.0	375	12	ADP22319	Adp22319 Human ant
39	316.4	83.0	375	12	ADP22327	Adp22327 Human ant
40	316.4	83.0	375	12	ADP22323	Adp22323 Human ant
41	316.4	83.0	376	10	ADL28450	AdL28450 Human ant
42	316.4	83.0	376	10	ADL28442	AdL28442 Human ant
43	316.4	83.0	437	6	ABL53510	AbL53510 Human rec
44	316.4	83.0	1413	10	ADL28466	AdL28466 Human ant
45	315.2	82.7	373	10	ADL28488	AdL28488 Human ant

ALIGNMENTS

RESULT 1	AAx77236	standard; DNA; 381 BP.
ID	AAx77236	
XX	AAx77236	
AC	AAx77236	
XX	AAx77236	
DT	04-AUG-1999	(first entry)
XX	04-AUG-1999	
DE	Human DA.5 heavy chain variable region encoding DNA.	
XX	Human DA.5 heavy chain variable region encoding DNA.	
KW	Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;	
KM	autoimmune disease; scFv-antibody; single-chain Fv; ss.	
OS	Homo sapiens.	
XX	Homo sapiens.	
PN	WO925818-A1.	
XX	WO925818-A1.	
PD	27-MAY-1999.	
XX	27-MAY-1999.	
PF	16-NOV-1998; 98WO-EP007313.	
XX	16-NOV-1998; 98WO-EP007313.	
PR	17-NOV-1997; 97EP-00120096.	
XX	17-NOV-1997; 97EP-00120096.	
PA	(KUFE/) KUFE P.	
XX	(KUFE/) KUFE P.	
PI	Kuifer P, Raum T, Borschert K, Zettl F, Lutterbuese R,	
XX	Kuifer P, Raum T, Borschert K, Zettl F, Lutterbuese R,	
DR	WPI; 1999-338004/28.	
XX	WPI; 1999-338004/28.	
PT	P-PSDB; AAV17954.	
XX	P-PSDB; AAV17954.	
PS	Phage display system for identification of binding site domains retaining	
XX	capacity to bind an epitope.	
XX	Phage display system for identification of binding site domains retaining	
XX	capacity to bind an epitope.	
XX	Disclosure; Fig 3.1; 152pp; English.	
CC	The invention relates to a method of identifying binding site domains	
CC	(BSD) that retain the capacity of binding to a predetermined epitope when	
CC	positioned C-terminal of at least one further domain in a recombinant bi-	
CC	or multivalent polypeptide. The method comprises (a) testing a panel of	
CC	BSD displayed on the surface of a biological display system as part of a	
CC	fusion protein for binding to a predetermined epitope, where the fusion	
CC	protein comprises an additional domain positioned N-terminal of the BSD	
CC	and an amino acid sequence that mediates anchoring of the fusion protein	
CC	to the surface of the display system; and (b) identifying a BSD that	

CC binds to the predetermined epitope. The method is useful to identify bi-
CC or multivalent polypeptides that comprise antibody binding sites capable
CC of efficiently binding to the corresponding antigen. The polypeptides or
CC antibodies identified by the method are useful therapeutically and
CC diagnostically, for e.g. cancer and autoimmune diseases. scFv-antibody
CC fragments that bind independently of their position within bifunctional
CC single-chain fusion proteins can be isolated from combinatorial antibody
CC libraries using the new in vitro method

XX Sequence 381 BP; 87 A; 93 C; 120 G; 81 T; 0 U; 0 Other;

Query Match 99.6%; Score 379.4; DB 2; Length 381;
Best Local Similarity 99.7%; Pred. No. 1.7e-100;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGGTGCACTGCTGAGTCTGAGGAGGCGCTGTCACGCTGGAGGTCCTGAGACTC 60
DB 1 GAGGTGCACTGCTGAGTCTGAGGAGGCGCTGTCACGCTGGAGGTCCTGAGACTC 60
QY 61 TCTGTGCAAGCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 120
DB 61 TCTGTGCAAGCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 120
QY 121 CAGGCAAGGCGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 180
DB 121 CAGGCAAGGCGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 180
QY 181 GCAAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 240
DB 181 GCAAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 240
QY 241 CTGCAATGAAACGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 300
DB 241 CTGCAATGAAACGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 300
QY 301 GGGTGGGCGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 360
DB 301 GGGTGGGCGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 360
QY 361 ACCACGCTACCGCTCTCTCA 381
DB 361 ACCACGCTACCGCTCTCTCA 381

RESULT 2

AAV68537 standard; DNA; 414 BP.

XX AAV68537;

XX 16-FEB-1999 (first entry)

DE Nucleotide sequence of human D4.5 heavy chain variable region.

XX Human; D4.5 heavy chain variable region; receptor; antigen; tumour;
KW auto-immune disease; graft rejection; allergy; inflammatory disease;
KW endocrine disease; degenerative disease; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 1..414 /tag= a /product= "human D4.5 heavy chain variable region"

XX WO9846645-A2.

XX 22-OCT-1998.

XX 14-APR-1998; 98WO-EP002180.

XX 14-APR-1997; 97EP-00106109.

XX

PA (KUPER/) KUPER P.
PA (RAUM/) RAUM T.
XX Kufer P, Raum T;
XX WPI: 1998-594564/50.
DR P-PsDB; AAW80815.
XX Production of anti-human antigen receptors - by selecting a combination
PT of functionally rearranged VH and VL immunoglobulin chains expressed from
PT a recombinant vector.
XX Claim 9; Fig 7; 84pp; English.

CC This is the nucleotide sequence of the human D4.5 heavy chain variable
CC region, used in the method of the invention, for providing receptors that
CC can be used for targeting antigens in humans without being immunogenic
CC themselves. Such receptors can be used for treating diseases such as
CC tumours or auto-immune diseases, graft rejection after transplantation,
CC infectious diseases by targeting cellular receptors as well as allergic,
CC inflammatory, endocrine and degenerative diseases by targeting key
CC molecules involved in the pathological process

XX Sequence 414 BP; 93 A; 106 C; 127 G; 88 T; 0 U; 0 Other;

Query Match 99.6%; Score 379.4; DB 2; Length 414;
Best Local Similarity 99.7%; Pred. No. 1.8e-100;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGGTGCACTGCTGAGTCTGAGGAGGCGCTGTCACGCTGGAGGTCCTGAGACTC 60
DB 1 GAGGTGCACTGCTGAGTCTGAGGAGGCGCTGTCACGCTGGAGGTCCTGAGACTC 60
QY 61 TCTGTGCAAGCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 120
DB 61 TCTGTGCAAGCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 120
QY 121 CAGGCAAGGCGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 180
DB 121 CAGGCAAGGCGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 180
QY 181 GCAAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 240
DB 181 GCAAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 240
QY 241 CTGCAATGAAACGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 300
DB 241 CTGCAATGAAACGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 300
QY 301 GGGTGGGCGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 360
DB 301 GGGTGGGCGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 360
QY 361 ACCACGCTACCGCTCTCTCA 381
DB 361 ACCACGCTACCGCTCTCTCA 381

RESULT 3

AAZ50588 standard; DNA; 1630 BP.

XX AAZ50588;

XX 23-MAY-2000 (first entry)

DE HD70scFv-Ck-interleukin 2 encoding DNA.

XX HD70; single-chain variable fragment; scFv; 17-1A antigen; human; BpCAM;
KW epithelial cell adhesion molecule; inflammatory cytokine; IL-2;
KW interleukin-2; Ck-domain; kappa light chain constant domain;
KW heteronucleotide; multifunctional compound; immunoglobulin; cyostatic;
KW immunostimulatory; anti-leukemia; diagnosis; prevention;

KW antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;
 KW leukaemia; solid tumour; carcinoma; melanoma; sarcoma; ds.
 OS Homo sapiens.
 XX
 XX
 FT Key Location/Qualifiers
 FT CDS 39..1613
 FT /tag= a
 FT /product= "HD70scFv-CK-IL-2 chain"
 FT misc_feature
 FT /tag= b
 FT /label= HD70_scFv
 XX
 XX
 PN WO200006605-A2.
 XX
 PD 10-FEB-2000.
 XX
 PF 28-JUL-1999; 99WO-EP005416.
 XX
 PR 28-JUL-1998; 98EP-00114082.
 XX
 PA (MCCR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
 PI Kufer P, Dreier T, Baerle PA, Borschert K, Zettl F;
 DR MPI; 2000-195265/17.
 XX P-PSDB; AAY44995.
 DR
 PT New multifunctional compounds useful for preventing and/or treating
 XX malignant cell growth and for detection and diagnosis.
 XX
 PS Claim 8; Fig 55B; 166pp; English.
 XX
 CC The patent discloses heteromimetics which are multifunctional compounds
 CC producible in a mammalian host cell as a secretable and fully functional
 CC heterodimer of two polypeptide chains, where one of the polypeptide
 CC chains comprises a CH1-domain (constant domain of an immunoglobulin
 CC heavy chain) and the other chain comprises a C-domain (constant domain of
 CC an immunoglobulin light chain). The polypeptide chains further comprise,
 CC fused to the constant domains at least two (poly)peptides having
 CC different receptor or ligand functions, where further at least two of the
 CC different (poly)peptides lack an intrinsic affinity for one another and
 CC are linked via the constant domains. The heteromimetics have
 CC cytostatic, immunostimulatory, antileukemia and antiproliferative
 CC activities. These compounds can be used for diagnosing, preventing and
 CC treating malignant cell growth related to malignancies of haematopoietic
 CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
 CC melanomas and sarcomas. The present sequence is a DNA encoding right
 CC chain of a heteromimetic comprising HD70 single-chain Fv (scFv) fragment
 CC N-terminally linked to human CK domain (constant domain of immunoglobulin
 CC -kappa light chain) which bears at its C-terminus the human inflammatory
 CC cytokine interleukin-2 (IL-2). HD70 scFv specifically recognises the
 CC human epithelial cell adhesion molecule (EPCAM) also called 17-1A antigen
 XX
 SQ Sequence 1630 BP; 445 A; 410 C; 408 G; 367 T; 0 U; 0 Other;
 Query Match 99.3%; Score 378.4; DB 3; Length 1630;
 Best Local Similarity 99.7%; Pred. No. 5.4e-100;
 Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GAAGTGAAGTGTCTGAGTCTGGGAGGAGGCTGTCCAGCTGGAGAGTCCGAGAGCTC 60
 DB 462 GAGGTGAGTGTCTGAGTCTGGGAGGAGGCTGTCCAGCTGGAGAGTCCGAGAGCTC 521
 QY 61 TCCTGTGAGAGCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 120
 DB 522 TCCTGTGAGAGCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 561
 QY 121 CCAAGGCAAGGGGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 180
 DB 582 CCAAGGCAAGGGGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 641
 QY 181 GCAAGCTCGGTGAAGGGCGCATTCACATCTCCAGAGACAAATTCAGAGAGAGCTGAT 240

DB 642 GCAGAGCTCGGTGAAGGGCGCATTCACATCTCCAGAGACAAATTCAGAGAGAGCTGAT 701
 QY 241 CTGCAATATGAACAGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 300
 DB 702 CTGCAATATGAACAGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 761
 QY 301 GGGTGGGGGAGTGGTGGAGACCTTACTACTAGTATGAGAGCTGGGGCCAAAGG 360
 DB 762 GGGTGGGGGAGTGGTGGAGACCTTACTACTAGTATGAGAGCTGGGGCCAAAGG 821
 QY 361 ACCAGGTGACCGTCTCTC 380
 DB 822 ACCAGGTGACCGTCTCTC 841
 RESULT 4
 AAZ50587
 ID AAZ50587 standard; DNA; 1630 BP.
 AC
 AC AAZ50587;
 XX
 DT 23-MAY-2000 (first entry)
 XX
 DE HD70scFv-CH1-GM-CSF chain encoding DNA.
 XX
 KW HD70; single-chain variable fragment; scFv; 17-1A antigen; human; EPCAM;
 KW epithelial cell adhesion molecule; inflammatory cytokine; GM-CSF;
 KW granulocyte/macrophage colony stimulating factor; heteromimetic;
 KW CH1-domain; multifunctional compound; heavy chain constant domain;
 KW immunoglobulin; cytostatic; immunostimulatory; antileukemia; diagnosis;
 KW antiproliferative; prevention; treatment; malignant; haematopoietic cell;
 KW lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma; ds.
 XX
 OS Homo sapiens.
 XX
 XX
 FT Key Location/Qualifiers
 FT CDS 39..1610
 FT /tag= a
 FT /product= "HD70scFv-CH1-GM-CSF chain"
 FT misc_feature
 FT /tag= b
 FT /label= HD70_scFv
 XX
 PN WO200006605-A2.
 XX
 PD 10-FEB-2000.
 XX
 PF 28-JUL-1999; 99WO-EP005416.
 XX
 PR 28-JUL-1998; 98EP-00114082.
 XX
 PA (MCCR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
 PI Kufer P, Dreier T, Baerle PA, Borschert K, Zettl F;
 DR MPI; 2000-195265/17.
 XX P-PSDB; AAY44994.
 DR
 PT New multifunctional compounds useful for preventing and/or treating
 XX malignant cell growth and for detection and diagnosis.
 XX
 PS Claim 8; Fig 55A; 166pp; English.
 XX
 CC The patent discloses heteromimetics which are multifunctional compounds
 CC producible in a mammalian host cell as a secretable and fully functional
 CC heterodimer of two polypeptide chains, where one of the polypeptide
 CC chains comprises a CH1-domain (constant domain of an immunoglobulin
 CC heavy chain) and the other chain comprises a C-domain (constant domain of
 CC an immunoglobulin light chain). The polypeptide chains further comprise,
 CC fused to the constant domains at least two (poly)peptides having
 CC different receptor or ligand functions, where further at least two of the
 CC different (poly)peptides lack an intrinsic affinity for one another and

CC are linked via the constant domains. The heteronucleotides have
CC cytosolic, immunostimulatory, antileukemia and antiproliferative
CC activities. These compounds can be used for diagnosing, preventing and
CC treating malignant cell growth related to malignancies of haematopoietic
CC cells e.g. lymphomas and leukemias, or to solid tumours e.g. carcinomas,
CC melanomas and sarcomas. The present sequence is a DNA encoding left chain
CC of a heteronucleotide comprising HD70 single-chain Fv (scFv) fragment N-
CC terminally linked to human CH1 domain which bears at its C-terminus the
CC human inflammatory cytokine granulocyte/macrophage colony stimulating
CC factor (GM-CSF), plus a hexanetidine sequence for ease of purification.
CC HD70 scFv specifically recognises the human epithelial cell adhesion
CC molecule (EPCAM) also called 17-1A antigen

Sequence 1630 BP; 376 A; 484 C; 437 G; 333 T; 0 U; 0 Other;

Query Match 99.3%; Score 378.4; DB 3; Length 1630;
Best Local Similarity 99.7%; Pred. No. 5.4e-100;
Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGGTGACAGTCTGAGTCTGGGGAGGCGTGTCCAGCTGGAGGTCCTGAGACTC 60
DB 462 GAGGTGACAGTCTGAGTCTGGGGAGGCGTGTCCAGCTGGAGGTCCTGAGACTC 521
QY 61 TCCTGTGACAGCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 120
DB 522 TCCTGTGACAGCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 581
QY 121 CCAGGCAAGAGGCGTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 180
DB 582 CCAGGCAAGAGGCGTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 641
QY 181 GCAGATCTCGTGTGAGGCGGATTCACATCTCCAGAGACATTCAGAGACGCTGTAT 240
DB 642 GCAGATCTCGTGTGAGGCGGATTCACATCTCCAGAGACATTCAGAGACGCTGTAT 701
QY 241 CTGCAATGAAACAGCTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 300
DB 702 CTGCAATGAAACAGCTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 761
QY 301 GGTGTGGGAGTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 360
DB 762 GGTGTGGGAGTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 821
QY 361 ACCAGGTGACGCTCTCTC 380
DB 822 ACCAGGTGACGCTCTCTC 841

RESULT 5
ID AAA46898 standard; DNA; 1413 BP.
XX AAA46898;

DT 03-OCT-2000 (first entry)

DE DNA encoding the heavy chain of immunoglobulin clone 11.2.1.

KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
KW proliferative disorder; cancer; immunodeficient disorder; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
XX CDS 58..1413
XX FT /*tag= a

XX MO200037504-A2.

XX 29-JUN-2000.

XX 23-DEC-1999; 99WO-US030895.

XX 23-DEC-1998; 98US-0113647P.

XX (PRTZ) PRIZER INC.
XX (ABGE-) ABGENIX INC.

XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
XX Corvalan JR;

XX WPI, 2000-442647/38.

XX F-PSDB; AAY93734.

XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
XX PT -4 containing specified heavy and light chain sequences, useful for
XX treating, e.g. immune disorders.

XX Example 2; Fig 22p; 157pp; English.

XX The present sequence encodes a heavy chain of an antibody of the
XX invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
XX -4. Antibodies of the invention are composed of a heavy chain variable
XX region, comprising a modified contiguous sequence from a FRI-FR3 sequence
XX encoded by a human VAI-33 family gene. The modifications are contained in
XX CDR1, CDR2 and/or framework regions. The antibodies may be used to
XX inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
XX disorders (e.g. autoimmune disease, diabetes and graft rejection) and
XX proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
XX used to up-regulate immune system to up-regulate immunodeficient
XX disorders

Sequence 1413 BP; 321 A; 437 C; 395 G; 260 T; 0 U; 0 Other;

Query Match 85.1%; Score 324.4; DB 3; Length 1413;
Best Local Similarity 92.9%; Pred. No. 2.9e-84;
Matches 353; Conservative 0; Mismatches 21; Indels 6; Gaps 1;

QY 2 AGTGCAGCTGCTGAGTCTGGGGAGGCGTGTCCAGCTGGAGGTCCTGAGACTCT 61
DB 59 AGTGCAGCTGCTGAGTCTGGGGAGGCGTGTCCAGCTGGAGGTCCTGAGACTCT 118
QY 62 CTTGTGACAGCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 121
DB 119 CTTGTGACAGCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 178
QY 122 CAGGCAAGGCGTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 181
DB 179 CAGGCAAGGCGTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 238
QY 182 CAGACTCGTGTGAGGCGGATTCACATCTCCAGAGACATTCAGAGACGCTGTATC 241
DB 239 CAGACTCGTGTGAGGCGGATTCACATCTCCAGAGACATTCAGAGACGCTGTATC 298
QY 242 TGCATATGAAACAGCTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 301
DB 299 TGCATATGAAACAGCTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 358
QY 302 GGTGTGGGAGTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 361
DB 359 GGTGTGGGAGTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 412
QY 362 CCAGGTGACGCTCTCTCA 381
DB 413 CCAGGTGACGCTCTCTCA 432

RESULT 6
ID AAD54349 standard; CDNA; 1413 BP.
XX AAD54349;

XX 17-JUN-2003 (first entry)

CC TNFa induced apoptosis by administering the human monoclonal antibody of
CC (I): (I) has anabolic, antiarteriosclerotic, antiarthritic,
CC antibacterial, antiinflammatory, antipneumatic, eating-
CC disorders, immunomodulator, immunosuppressive, nephrotropic,
CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
CC as a TNFa antagonist. The antibody (I) is useful in the preparation of
CC medicament for treating TNF induced apoptosis, neoplastic disease such as
CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
CC diseases such as rheumatoid arthritis, glomerulonephritis,
CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
CC multiple sclerosis. The present sequence encodes a human anti-TNfa
CC antibody light chain variable region, which is used in the
CC exemplification of the present invention.

XX SQ Sequence 378 BP; 85 A; 92 C; 120 G; 81 T; 0 U; 0 Other;

Query Match 85.0%; Score 324; DB 12; Length 378;
Best Local Similarity 92.6%; Pred. No. 2.5e-84;
Matches 352; Conservative 0; Mismatches 25; Indels 3; Gaps 1;

QY 2 AGGTGACGCTGCTCGAGTCTGGGGAGGCGCTGGTCCAGCTGGAGAGTCCCTGAGACTCT 61
DB 2 AGGTGACGCTGCTGGAGTCTGGGGAGGCGCTGGTCCAGCTGGAGAGTCCCTGAGACTCT 61
QY 62 CCTGTGACGCTCTTGATTCACCTTCACTGATGATGATGATGATGATGATGATGATGATG 121
DB 62 CCTGTGACGCTCTTGATTCACCTTCACTGATGATGATGATGATGATGATGATGATGATG 121
QY 122 CAGGCAAGGGGCTGGAGTGGGGTGGAGTATATCATATATATATATATATATATATATG 181
DB 122 CAGGCAAGGGGCTGGAGTGGGGTGGAGTATATATATATATATATATATATATATATG 181
QY 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGAACAGCGCTGATC 241
DB 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGAACAGCGCTGATC 241
QY 242 TGCATATGAACACCTGAGAGCTGAGAGACACCGCTGTGATTACTGTGGAAAGATATG 301
DB 242 TGCATATGAACACCTGAGAGCTGAGAGACACCGCTGTGATTACTGTGGAAAGATATG 301
QY 302 GGTGGGGCAGTGGCTGAGAGACCTACTACTACTAGGATGAGCGTCTGGGGCCAAAGGA 361
DB 299 GGTGGGGCAGTGGCTGAGAGACCTACTACTACTAGGATGAGCGTCTGGGGCCAAAGGA 361
QY 362 CCACGGTCAACCGTCTCTCTCA 381
DB 359 CCACGGTCAACCGTCTCTCTCA 378

RESULT 8
ADK18651
ID ADK18651 standard; DNA; 382 BP.

AC ADK18651;

DT 06-MAY-2004 (first entry)

XX Anti-human PDGF-D antibody heavy chain gene sequence.

KW ds; gene; antiinflammatory; immunomodulator; cyostatic; gene therapy.

OS Homo sapiens.

XX WO2003057857-A2.

PD 17-JUL-2003.

PF 06-JAN-2003; 2003WO-US000398.

XX 07-JAN-2002; 2002US-00041860.

XX (ABGE-) ABGENIX INC.
PA Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX WPI; 2003-587119/55.

PT New human monoclonal antibody that binds to platelet-derived growth
PT factor-D (PDGF-D), useful for treating chronic and recurrent human
PT diseases, such as inflammation, autoimmunity and cancer.

PS Disclosure; SEQ ID NO 75; 255pp; English.

CC The invention relates to a human monoclonal antibody that binds to
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC treating chronic and recurrent human diseases, such as inflammation,
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC useful for modulating collagen formation, and for staging various
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC generated using an active protein fragment of the gene product from the
CC clone 30664188.0.99 arising in the conditioned medium obtained when
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC sequence corresponds to a DNA used in the invention.

XX SQ Sequence 382 BP; 88 A; 90 C; 118 G; 86 T; 0 U; 0 Other;

Query Match 85.0%; Score 324; DB 10; Length 382;
Best Local Similarity 90.8%; Pred. No. 2.5e-84;
Matches 345; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 2 AGGTGACGCTGCTGAGTCTGGGGAGGCGCTGGTCCAGCTGGAGAGTCCCTGAGACTCT 61
DB 2 AGGTGACGCTGCTGAGTCTGGGGAGGCGCTGGTCCAGCTGGAGAGTCCCTGAGACTCT 61
QY 62 CCTGTGACGCTCTTGATTCACCTTCACTGATGATGATGATGATGATGATGATGATGATG 121
DB 62 CCTGTGACGCTCTTGATTCACCTTCACTGATGATGATGATGATGATGATGATGATGATG 121
QY 122 CAGGCAAGGGGCTGGAGTGGGGTGGAGTATATCATATATATATATATATATATATATG 181
DB 122 CAGGCAAGGGGCTGGAGTGGGGTGGAGTATATATATATATATATATATATATATATG 181
QY 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGAACAGCGCTGATC 241
DB 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGAACAGCGCTGATC 241
QY 242 TGCATATGAACACCTGAGAGCTGAGAGACACCGCTGTGATTACTGTGGAAAGATATG 301
DB 242 TGCATATGAACACCTGAGAGCTGAGAGACACCGCTGTGATTACTGTGGAAAGATATG 301
QY 302 GGTGGGGCAGTGGCTGAGAGACCTACTACTACTAGGATGAGCGTCTGGGGCCAAAGGA 361
DB 302 ACTATGATATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATG 361
QY 362 CCACGGTCAACCGTCTCTCTCA 381
DB 362 CCACGGTCAACCGTCTCTCTCA 381

RESULT 9
ADL25435
ID ADL25435 standard; cDNA; 382 BP.

AC ADL25435;

DT 17-JUN-2004 (first entry)

DE Human mAb 1.38.1 heavy chain variable region encoding cDNA SEQ ID NO:45.

XX antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;
KW nephritis; mesangial cell proliferation inhibition;
KW mesangial proliferative glomerulonephritis; nephrotropic;

KM		antiinflammatory; dermatological; immunosuppressive; antidiabetic;
RN		gene therapy; human; monoclonal antibody; mab; gene; ss.
XX	Homo sapiens.	
OS		
XX	Key	Location/Qualifiers
FH	CDS	1..381
FT		/tag= a
PT		/product= "mab 1.38.1 heavy chain variable region"
XX	WO2004024098-A2.	
FN		
XX	PD	25-MAR-2004 .
PD		
PP		
PF		16-SEP-2003; 2003WO-US029414.
XX		
PR		16-SEP-2002; 2002US-041137P.
XX		
PA	(ABGE-) ABGENIX INC. (CURA-) CURAGEN CORP.	
XI		
P1	Floege J , Gazit-Bornstein G, Keyt B, Larochele WJ, Lichtenstein H,	
XX		
DR	WPI : 2004-269881/25.	
DR	P-PADB; ADL25436.	
XX		
XT		
PT	Use of an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD) for preparing a medicament for treating nephritis.	
PT		
PS	Disclosure; SEQ ID NO 45; 115pp; English.	
XX		
CC	The present invention describes an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD), where the antibody is useful in preparing a medicament for treating nephritis. Also described: (1) a method of detecting nephritis; (2) a method of treating nephritis; (3) a method of inhibiting mesangial cell proliferation; and (4) a method of treating mesangial proliferative glomerulonephritis. The antibody has neurotrophic, anti-inflammatory, dermatological, immunosuppressive and antibacterial activities, and can be used in gene therapy. The antibody or its binding fragment, that binds PDGF-DD, can be used in preparing a medicament for treating nephritis and related disorders, e.g., mesangial proliferative glomerulonephritis. The present sequence encodes a human monoclonal antibody (mAb) variable region sequence, which is used in the exemplification of the present invention.	
CC		
CC		
SQ	Sequence 382 BP; 88 A; 90 C; 118 G; 86 T; 0 U; 0 Other;	
Query Match	85.0%; Score 324; DB 12; Length 382;	
Best Local Similarity	90.8%; Pred. No. 2.5e-84;	
Matches 345; Conservative	0; Mismatches 35; Indels 0; Gaps 0;	
OY	AGGTCACCTGGTGCAGGTCTTGCGGGAGGCCCTGGTCACGCTGGGAGGTCCCGAGAATCT	61
Dbb	2 AGGTCACCTGGTGCAGGTCTTGCGGGAGGCCCTGGTCACGCTGGGAGGTCCCGAGAATCT	61
OY	CCTGTGCACCCTCTTGATTCACTTTCAGTAGCTATGGAATGACTGGGTCGCCAGGCTC	121
Ddb	62 CCTGTGCACCCTCTTGATTCACTTTCAGTAGCTATGGAATGACTGGGTCGCCAGGCTC	121
OY	CAGGCAAGGGGCTGGAGTGGGTGGCGATTATATCATATGATGAAGATAATTAATATCTATG	181
Ddb	122 CAGGCAAGGGGCTGGAGTGGGTGGCGATTATATCATATGATGAAGATAATTAATATCTATG	181
OY	CAGACTCCGTGAAGGGCCGATTCAACAATCTCCAGAGAACAAATTCCAAAGAACGGCTGATC	241
Ddb	182 CAGACTCCGTGAAGGGCCGATTCAACAATCTCCAGAGAACAAATTCCAAAGAACGGCTGATC	241
OY	TGCAATTAACACGCTTGAGAGCTGAGACAACGGCTGTGATTACTGTGCGAAAATATG	301
Ddb	242 TGCAATTAACACGCTTGAGAGCTGAGACAACGGCTGTGATTACTGTGCGAGAAGATAT	301
OY	GGTGGGGCAGTGGCTTGAGAACCTTACTACTAGCTATGAGACGTCTGGGGCCAAGGGA	361

Db	302	ACATATATAGTAGTATATCTCTACTACTACTA	CTAAGGATGACCTCTGGGCCAAGGA	361
Oy	362	CCACGGTCACCGTCTCTCTCA	381	
Db	362	CCACGGTCACCGTCTCTCTCA	381	
RESULT 10				
ADP22135				
ID	ADP22135	standard;	CDNA;	372 BP.
AC				
XX	ADP22135;			
DT	09-SEP-2004	(first entry)		
XX				
DE	Human anti-TNFa antibody heavy chain variable region	CDNA SEQ ID NO:41.		
XX				
KW	human; monoclonal antibody; tumour necrosis factor-alpha; TNFalpha;			
KW	anti-TNFa antibody; anabolic; antihypertensive; antirheumatic;			
KW	antibacterial; antiinflammatory; antiparasitic; antineoplastic;			
KW	eating-disorder; immunomodulator; immunosuppressive; nephrotropic;			
KW	neuroprotective; vasotropic; antiapoptotic; TNFalpha antagonist;			
KW	TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer			
KW	bladder cancer; lung cancer; glioblastoma; stomach cancer;			
KW	endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;			
KW	prostate cancer; immuno-mediated inflammatory disease;			
KW	rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;			
KW	resterosis; autoimmune disease; Crohn's disease; graft-host reaction;			
XX	septic shock; cachexia; anorexia; multiple sclerosis; gene; ss.			
XX				
OS	Homo sapiens.			
XX				
XX				
FH	Key	Location/Qualifiers		
FT	CDS	1..372		
FT		/*tag= a		
FT		/product= "human anti-TNFa antibody heavy chain variable		
FT		region"		
XX				
XX	WO2004050683-A2.			
XX				
PD	17-JUN-2004.			
XX				
XX	02-DEC-2003; 2003WO-US038281.			
XX				
PR	02-DEC-2002; 2002US-0430729P.			
XX				
PA	(ABGE-) ABGENIX INC.			
XX				
P1	Babcock JS, Kang JS, Foord O, Green LJ, Feng X, Klakamp S;			
P1	Haak-Frendescho M, Rathanaswami P, Pigott C, Liang ML, Lee R;			
P1	Manchulenchko K, Faggioni R, Senaldi G, Qiaojuan JS;			
XX				
XX	WPI, 2004-480601/45.			
DR	P-PSDB; ADP22136.			
XX				
PT	New recombinant human monoclonal antibody that specifically binds to			
PT	Tumour Necrosis Factor-alpha, useful for treating neoplastic disease such			
PT	as cancers, or immuno-mediated inflammatory diseases such as rheumatoid			
PT	arthritis.			
XX				
XX				
PS	Example 10; SEQ ID NO 41; 213pp; English.			
XX				
CC	The present invention describes a human monoclonal antibody (I) that			
CC	specifically binds to tumour necrosis factor-alpha (TNFalpha) and comprises:			
CC	(a) a heavy chain complementarily determining region 1 (CDR1) having the			
CC	two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421)			
CC	and (b) a light chain CDR1 having the two fully defined 11 amino acid			
CC	sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying			
CC	(M1) the level of TNFalpha in a patient sample, comprising contacting with			
CC	(1), and detecting the level of binding between the antibody and TNFalpha in			
CC	the sample; (2) a composition comprising the antibody or its functional			
CC	fragment and a carrier; (3) treating (M2) an animal suffering from a			

neoplastic, or an immuno-mediated inflammatory disease by selecting an animal in need of treatment for the disease by administering the human monoclonal antibody of (1); and (4) inhibiting (M3) TNF α induced apoptosis in an animal by selecting an animal in need of treatment for TNF α induced apoptosis by administering the human monoclonal antibody of (1). (1) has anabolic, antiarteriosclerotic, antiarthritic, anti-infective, antiinflammatory, antipneumonic, antineurotic, eating-disorders, immunomodulatory, immunosuppressive, nephrotropic, neuroprotective, vasotropic and antiapoptotic activities, and can be used as a TNF α antagonist. The antibody (1) is useful in the preparation of a medicament for treating TNF induced apoptosis, neoplastic disease such as breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma, stomach cancer, endometrial cancer, kidney cancer, colon cancer, pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory diseases such as rheumatoid arthritis, glomerulonephritis, atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's disease, graft-host reactions, septic shock, cachexia, anorexia, and multiple sclerosis. The present sequence encodes a human anti-TNF α antibody heavy chain variable region, which is used in the exemplification of the present invention.

Sequence 372 BP; 85 A; 89 C; 115 G; 83 T; 0 U; 0 Other;

Query Match 84.8%; Score 323.2; DB 12; Length 372;
Best Local Similarity 92.9%; Pred. No. 4.2e-84;
Matches 353; Conservative 0; Mismatches 18; Indels 9; Gaps 1;

```
QY 2 AGGTGAGCTGCTGAGTCTGGGGAGGCTGCTGCAAGCTGGAGGCTCTGAGACTCT 61
    |||||
DB 2 AGGTGAGCTGCTGAGTCTGGGGAGGCTGCTGCAAGCTGGAGGCTCTGAGACTCT 61
    |||||
QY 62 CTTGTGAGCTCTGTGATTCACCTTCAGTATGATGATGATGATGATGATGATGATG 121
    |||||
DB 62 CTTGTGAGCTCTGTGATTCACCTTCAGTATGATGATGATGATGATGATGATGATG 121
    |||||
QY 122 CAGGCAAGGGGCTGGAGTGGGCTGATATCATATGATGATGATGATGATGATGATG 181
    |||||
DB 122 CAGGCAAGGGGCTGGAGTGGGCTGATATCATATGATGATGATGATGATGATGATG 181
    |||||
QY 182 CAGACTCCGTGAAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGAACGCTGTATC 241
    |||||
DB 182 CAGACTCCGTGAAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGAACGCTGTATC 241
    |||||
QY 242 TGCAGATGAAACGCTGAGAGCTGAGAGACCGGCTGTGTATTCCTGTGGAAGATATG 301
    |||||
DB 242 TGCAGATGAAACGCTGAGAGCTGAGAGACCGGCTGTGTATTCCTGTGGAAGATATG 301
    |||||
QY 302 GGTGGGGAGTGGCTGAGAGACCTTACTACTACGATATGAGAGCTGTGGGGCCAGAGGA 361
    |||||
DB 302 GGTGGGGAGTGGCTGAGAGACCTTACTACTACGATATGAGAGCTGTGGGGCCAGAGGA 361
    |||||
QY 362 CCAAGGTACCGTCTCTCA 381
    |||||
DB 362 CCAAGGTACCGTCTCTCA 381
    |||||
QY 353 CCAAGGTACCGTCTCTCA 372
    |||||
DB 353 CCAAGGTACCGTCTCTCA 372
    |||||
```

RESULT 11

AAA13939 standard; DNA; 429 BP.

AAA13939;

02-AUG-2000 (first entry)

Human PTHrP monoclonal antibody clone 5B12-16-12 DNA SEQ ID NO:41.

Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
fracture; cachexia; tooth disease; periodontal disease; gingivitis; sepsis;
systemic inflammatory response syndrome; SIRS; hypophosphataemia;
antiarthritic; cytostatic; antiinflammatory; ds.

Homo sapiens.

JP2000080100-A.
21-MAR-2000.
12-OCT-1998; 98JP-00304793.
17-JUN-1998; 98JP-00188196.
26-JUN-1998; 98JP-00196729.
(NIBS) JAPAN TOBACCO INC.
WPI; 2000-286723/25.
P-PDB; AAY82629.

A human monoclonal antibody to parathyroid hormone related protein. -
PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
including metastasis, and pain.

Example 10; Page 76; 88pp; Japanese.

The present invention describes a human monoclonal antibody to
parathyroid hormone related protein (PTHrP). The monoclonal antibody or
its fragments, following the stimulation of PTHrP has the following
properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
the release of calcium from bone; or (c) inhibits elevation of blood
calcium content. The monoclonal antibody can be used in the treatment of
hypercalcaemia, rheumatoid arthritis, cancer of bone including
metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
diseases and gingivitis, sepsis, systemic inflammatory response syndrome
(SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
antiinflammatory activities. The present sequence represents a human
PTHrP monoclonal antibody clone nucleotide sequence from the present
invention

Sequence 429 BP; 92 A; 99 C; 138 G; 100 T; 0 U; 0 Other;

Query Match 84.8%; Score 323.2; DB 3; Length 429;
Best Local Similarity 92.9%; Pred. No. 4.4e-84;
Matches 353; Conservative 0; Mismatches 18; Indels 9; Gaps 1;

```
QY 2 AGGTGAGCTGCTGAGTCTGGGGAGGCTGCTGCAAGCTGGAGGCTCTGAGACTCT 61
    |||||
DB 59 AGGTGAGCTGCTGAGTCTGGGGAGGCTGCTGCAAGCTGGAGGCTCTGAGACTCT 118
    |||||
QY 62 CTTGTGAGCTCTGTGATTCACCTTCAGTATGATGATGATGATGATGATGATGATG 121
    |||||
DB 119 CTTGTGAGCTCTGTGATTCACCTTCAGTATGATGATGATGATGATGATGATGATG 178
    |||||
QY 122 CAGGCAAGGGGCTGGAGTGGGCTGATATCATATGATGATGATGATGATGATGATG 181
    |||||
DB 179 CAGGCAAGGGGCTGGAGTGGGCTGATATCATATGATGATGATGATGATGATGATG 238
    |||||
QY 182 CAGACTCCGTGAAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGAACGCTGTATC 241
    |||||
DB 239 TAGACTCCGTGAAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGAACGCTGTATC 298
    |||||
QY 242 TGCAGATGAAACGCTGAGAGCTGAGAGACCGGCTGTGTATTCCTGTGGAAGATATG 301
    |||||
DB 299 TGCAGATGAAACGCTGAGAGCTGAGAGACCGGCTGTGTATTCCTGTGGAAGATATG 355
    |||||
QY 302 GGTGGGGAGTGGCTGAGAGACCTTACTACTACGATATGAGAGCTGTGGGGCCAGAGGA 361
    |||||
DB 356 -----GAGTGGCTGTGAGAGACCTTACTACTACGATATGAGAGCTGTGGGGCCAGAGGA 409
    |||||
QY 362 CCAAGGTACCGTCTCTCA 381
    |||||
DB 410 CCAAGGTACCGTCTCTCA 429
    |||||
```

RESULT 12

ADP22315 standard; cDNA; 375 BP.

XX AC ADP22315;
XX DT 09-SEP-2004 (first entry)
DE Human anti-TNFA antibody heavy chain variable region cDNA SEQ ID NO:221.
XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
XX anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;
XX antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
XX eating-disorder; immunomodulatory; immunosuppressive; nephrotoxic;
XX neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;
XX TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
XX bladder cancer; lung cancer; glioblastoma; stomach cancer;
XX endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
XX prostate cancer; immuno-mediated inflammatory disease;
XX rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
XX resenosis; autoimmune disease; Crohn's disease; graft-host reaction;
XX septic shock; cachexia; anorexia; multiple sclerosis; gene; ss.
OS Homo sapiens.
FH Location/Qualifiers
FT CDS 1..375
FT /tag= a
FT /product= "human anti-TNFA antibody heavy chain variable
FT region"
PN WO2004050683-A2.
XX 17-JUN-2004.
XX 02-DEC-2003; 2003WO-US038281.
XX 02-DEC-2002; 2002US-0430729P.
XX (ABGE-) ABGENIX INC.
XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
XX Haak-Frendscho M, Rathnaswami P, Pigott C, Liang WL, Lee R;
XX Manchulenko K, Faggitoni R, Senaldi G, Qiaojuan JS;
XX WPI, 2004-480601/45.
XX P-PSDB; ADP22316.
XX New recombinant human monoclonal antibody that specifically binds to
XX Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
XX as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
XX arthritis.
XX Example 10; SEQ ID NO 221; 213bp; English.
XX The present invention describes a human monoclonal antibody (I) that
XX specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
XX (a) a heavy chain complementarily determining region 1 (CDRI) having the
XX two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
XX and (b) a light chain CDRI having the two fully defined 11 amino acid
XX sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
XX (M1) the level of TNFa in a patient sample, comprising contacting with
XX (I), and detecting the level of binding between the antibody and TNFa in
XX the sample; (2) a composition comprising the antibody or its functional
XX fragment and a carrier; (3) treating (M2) an animal suffering from a
XX neoplastic, or an immuno-mediated inflammatory disease by selecting an
XX animal in need of treatment for the disease by administering the human
XX monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced
XX apoptosis in an animal by selecting an animal in need of treatment for
XX TNFa induced apoptosis by administering the human monoclonal antibody of
XX (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
XX antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
XX disorders, immunomodulatory, immunosuppressive, nephrotoxic, CC
XX neuroprotective, vasotropic and antiapoptotic activities, and can be used
XX as a TNFa antagonist. The antibody (I) is useful in the preparation of
XX medicament for treating TNF induced apoptosis, neoplastic disease such as

CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
CC diseases such as rheumatoid arthritis, glomerulonephritis,
CC atherosclerosis, psoriasis, resenosis, autoimmune disease, Crohn's
CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
CC multiple sclerosis. The present sequence encodes a human anti-TNFA
CC antibody heavy chain variable region, which is used in the
CC exemplification of the present invention.
XX
XX Sequence 375 BP; 87 A; 92 C; 116 G; 80 T; 0 U; 0 Other;
XX
XX Query Match 84.7%; Score 322.8; DB 12; Length 375;
XX Best Local Similarity 92.6%; Pred. No. 5,5e-84;
XX Matches 352; Conservative 0; Mismatches 22; Indels 6; Gaps 1;
QY 2 AGGTGACGTGCTGCGAGTCTGGGGAGAGCGCTGTCAGCTGGAGAGTCCGAGACTCT 61
DB 2 AGGTGACGTGCTGCGAGTCTGGGGAGAGCGCTGTCAGCTGGAGAGTCCGAGACTCT 61
QY 62 CCGTGCAGCCTCTGTGATTCACCTTCAGTATGACATGCACTGGGTCGCGAGGCTC 121
DB 62 CCGTGCAGCCTCTGTGATTCACCTTCAGTATGACATGCACTGGGTCGCGAGGCTC 121
QY 122 CAGGCAAGGGGCTGAGTGGGGGTGGGAGTATATGATGATGAGTAAATGATG 181
DB 122 CAGGCAAGGGGCTGAGTGGGGGTGGGAGTATATGATGATGAGTAAATGATG 181
QY 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAGACGCTGTATC 241
DB 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAGACGCTGTATC 241
QY 242 TCGAATGAACAGCTGAGAGCTGAGAGACAGCGCTGTATTAATCTGTGGAATATG 301
DB 242 TCGAATGAACAGCTGAGAGCTGAGAGACAGCGCTGTATTAATCTGTGGAATATG 301
QY 302 GGTGGGGCAGTGGCTGAGACACCTCTACTACTAGGTATGACGCTGGGGCGAAGGA 361
DB 302 GGTGGGGCAGTGGCTGAGACACCTCTACTACTAGGTATGACGCTGGGGCGAAGGA 361
QY 362 CCAGGGTCACCGTCTCTCTCA 381
DB 362 CCAGGGTCACCGTCTCTCTCA 381
QY 356 CCAAGGTCAACGCTCTCTCA 375
DB 356 CCAAGGTCAACGCTCTCTCA 375
RESULT 13
ADK18643
XX ID ADK18643 standard; DNA; 379 BP.
XX
XX ADK18643;
XX
XX 06-MAY-2004 (first entry)
XX
DE Anti-human PDGF-D antibody heavy chain gene sequence.
XX ds; gene; antiinflammatory; immunomodulator; cyrostatic; gene therapy.
XX Homo sapiens.
XX OS
XX PN WO2003057857-A2.
XX
XX 17-JUL-2003.
XX
XX 06-JAN-2003; 2003WO-US000398.
XX
XX 07-JAN-2002; 2002US-00041860.
XX
XX (ABGE-) ABGENIX INC.
XX Corvelan JFF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
XX Bezabeh B;
XX WPI, 2003-587119/55.
XX

RESULT 15

AA03436
ID AA03436 standard; cDNA, 381 BP.

XX AC AA03436;

XX DT 29-APR-2001 (first entry)

DE DNA encoding anti-adipocyte monoclonal antibody heavy chain, FAT 25.

XX KW Antibody; adipocyte; heavy chain; light chain; obesity; FAT;
heart disease; complementarity determining region; CDR; ss.

XX OS Homo sapiens.

XX WO00127279-A1.

XX PD 19-APR-2001.

XX PF 11-OCT-2000; 2000WO-GB003900.

XX PR 12-OCT-1999; 99US-0158812P.

XX PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Edwards BM, Main SH, Vaughan TJ;

XX DR WPI; 2001-282031/29.

XX DR P-PSDB; AAU02536.

PT Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.

XX PS Disclosure; Page 114; 182zp; English.

CC AA03401-AA03535 represent anti-adipocyte monoclonal antibody heavy and
CC light chain coding sequences of the invention. The antibodies can be used
CC in the treatment of obesity and obesity related diseases. The antibodies
CC can be used to deliver drugs or pro-drugs directly to the fat mass of an
CC obese patient or the antibody can be used as a therapeutic itself.
CC Antibodies binding specifically to adipocytes can be used to activate the
CC immune system to destroy the cells by complement mediated lysis. The
CC antibodies may be labeled with a detectable label such as radiolabel,
CC fluorescent or chemical group and used in methods of diagnosis in human
CC subjects e.g. to determine the presence of adipocyte antigen on the
CC surface of an adipocyte to detect or determine the presence or level of
CC adipocytes in a cell or tissue sample. The antibodies can be used as an
CC alternative means of treatment for obese patients other than undergoing
CC surgery to remove excess fat. Antibodies for different types of fat
CC deposits can also be produced e.g. intra-abdominal fat associated with
CC heart disease

SQ Sequence 381 BP; 87 A; 89 C; 122 G; 83 T; 0 U; 0 Other;

Query Match 84.5%; Score 321.8; DB 4; Length 381;

Best Local Similarity 90.3%; Pred.No. 1.1e-83;

Matches 344; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 GAGGTGACGCTCTGAGTCTGGGGAGGCGCTGGTCCAGCTGGGAGGTCCTTGAGACTC 60
DB 1 GAGGTGACGCTCTGAGTCTGGGGAGGCGCTGGTCCAGCTGGGAGGTCCTTGAGACTC 60
QY 61 TCTGTGACGCTCTGAGTCTGATTCACCTTCACTAGCTATGGCATGCACTGGGTCCGAGGCT 120
DB 61 TCTGTGACGCTCTGAGTCTGATTCACCTTCACTAGCTATGGCATGCACTGGGTCCGAGGCT 120
QY 121 CCAAGCAGAGGCGCTGAGTGGGTGGAGTTATATCATATGATGAAGTAATAATATAT 180
DB 121 CCAAGCAGAGGCGCTGAGTGGGTGGAGTTATATCATATGATGAAGTAATAATATAT 180
QY 181 GCAGACTCGTGAAGGCGGATTCACTCTCAGAGCAATTCACAGAACACGCTGTAT 240

DB 181 GCAGACTCGTGAAGGCGGATTCACTCTCAGAGCAATTCACAGAACACGCTGTAT 240
QY 241 CTGCAATGTAACAGCGCTGAGAGCTGAGACACAGCGCTGTATTAATGTCGAAAGATATG 300
DB 241 CTGCAATGTAACAGCGCTGAGAGCTGAGAGCACAGCGCTGTATTAATGTCGAAAGATG 300
QY 301 GGGTGGGCACTGCTGAGAGACCTTACTACTACGATATGAGCGTCTGGGGCCAAAGG 360
DB 301 TATGTGGCAGTGTATTATGGGCCACTTCTACTCATGAGACGCTGGGGCCAAAGG 360
QY 361 ACCACGTCACCGCTCTCTCA 381
DB 361 ACCAAGTCAACCGTCTCTCA 381

Search completed: December 7, 2004, 06:41:26
Job time : 324.553 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 05:42:24 ; Search time 78.6581 Seconds
(without alignments)
3442.884 Million cell updates/sec

Title: US-09-403-107-143_COPY_1_381

Perfect score: 381
Sequence: 1 gaggtgcagcgcgtcgagtc.....ccagcgtcacgctccctcca 381

Scoring table:
IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/prodata/1/ina/6CTUS_COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	324.4	85.1	1413	4	US-09-472-087-61 Sequence 61, Appl
2	313.8	82.4	378	3	US-09-240-274-95 Sequence 95, Appl
3	310.6	81.5	378	3	US-09-240-274-94 Sequence 94, Appl
4	310.6	81.5	378	3	US-09-240-274-196 Sequence 196, Appl
5	308.8	81.0	372	4	US-09-424-840-15 Sequence 15, Appl
6	307.6	80.7	369	4	US-09-424-840-5 Sequence 5, Appl
7	304.2	79.8	378	3	US-09-240-274-195 Sequence 195, Appl
8	301	79.0	378	3	US-09-240-274-189 Sequence 189, Appl
9	300.4	78.8	867	3	US-08-862-124-16 Sequence 16, Appl
10	300.4	78.8	918	3	US-08-862-124-15 Sequence 15, Appl
11	300.4	78.8	918	3	US-08-862-124-13 Sequence 13, Appl
12	299.6	78.6	369	4	US-09-560-198A-1 Sequence 1, Appl
13	299.4	78.6	381	3	US-09-240-274-87 Sequence 87, Appl
14	298.8	78.4	867	3	US-08-862-124-14 Sequence 14, Appl
15	297.8	78.2	378	3	US-09-240-274-86 Sequence 86, Appl
16	296.4	77.8	503	4	US-09-472-087-35 Sequence 35, Appl
17	296.2	77.7	381	3	US-09-240-274-88 Sequence 88, Appl
18	295.8	77.6	512	3	US-09-545-809A-30 Sequence 30, Appl
19	294.2	77.2	369	4	US-09-560-198A-3 Sequence 3, Appl
20	293.2	77.0	369	4	US-09-560-198A-9 Sequence 9, Appl
21	291.4	76.5	381	3	US-09-240-274-182 Sequence 182, Appl
22	289.8	76.1	378	3	US-09-240-274-84 Sequence 84, Appl
23	289.8	76.1	378	3	US-09-240-274-85 Sequence 85, Appl
24	288.6	75.7	375	3	US-09-240-274-183 Sequence 183, Appl
25	288.2	75.4	378	3	US-09-240-274-83 Sequence 83, Appl
26	287.2	75.4	562	4	US-09-472-087-38 Sequence 38, Appl
27	287	75.3	372	3	US-09-240-274-73 Sequence 73, Appl

28	286.6	75.2	378	3	US-09-240-274-190 Sequence 190, Appl
29	285.8	75.0	372	3	US-09-240-274-74 Sequence 74, Appl
30	285.4	74.9	375	3	US-09-240-274-89 Sequence 89, Appl
31	285	74.8	378	3	US-09-240-274-79 Sequence 79, Appl
32	285	74.8	378	3	US-09-240-274-187 Sequence 187, Appl
33	285	74.8	381	3	US-09-240-274-188 Sequence 188, Appl
34	284.8	74.8	384	3	US-09-240-274-70 Sequence 70, Appl
35	284.4	74.6	342	2	US-08-477-552A-53 Sequence 53, Appl
36	284.2	74.6	372	3	US-09-240-274-71 Sequence 71, Appl
37	284.2	74.6	372	3	US-09-240-274-75 Sequence 75, Appl
38	283.8	74.5	375	3	US-09-240-274-90 Sequence 90, Appl
39	283.4	74.4	378	3	US-09-240-274-193 Sequence 193, Appl
40	283.2	74.3	384	3	US-09-240-274-185 Sequence 185, Appl
41	282.8	74.2	375	3	US-09-240-274-91 Sequence 91, Appl
42	282.6	74.2	372	3	US-09-240-274-76 Sequence 76, Appl
43	282.2	74.1	372	3	US-09-240-274-77 Sequence 77, Appl
44	281.4	73.9	583	3	US-08-545-809A-33 Sequence 33, Appl
45	280.8	73.7	933	3	US-09-079-029-8 Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-472-087-61
Sequence 61, Application US/09472087

Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, EILEEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PFI
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 61
LENGTH: 1413
TYPE: DNA
ORGANISM: Homo sapiens
US-09-472-087-61

Query Match 85.1%; Score 324.4; DB 4; Length 1413;
Best Local Similarity 92.9%; Pred. No. 36-93;
Matches 353; Conservative 0; Mismatches 21; Indels 6; Gaps 1;

QY	2	AGGTGAGTGTGCTGAGTGTGGGGAGGCGTGTGAGGCTGAGGCTGAGTGTG	61
DB	59	AGGTGAGTGTGCTGAGTGTGGGGAGGCGTGTGAGGCTGAGGCTGAGTGTG	118
QY	62	CTGTGACAGCTCTGTGATTCACCTTCAGTATGATGATGATGATGATGATG	121
DB	119	CTGTGACAGCTCTGTGATTCACCTTCAGTATGATGATGATGATGATGATG	178
QY	122	CAGGCAAGGGGCTGAGTGTGGGAGGCTGATATCATATGATGATGATGATG	181
DB	179	CAGGCAAGGGGCTGAGTGTGGGAGGCTGATATCATATGATGATGATGATG	238
QY	182	CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACATTCAGAGACGCT	241
DB	239	CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACATTCAGAGACGCT	298
QY	242	TGCATATGAACAGCTGAGAGTGAAGACAGGCTGTGTATTAATGATGATG	301
DB	299	TGCATATGAACAGCTGAGAGTGAAGACAGGCTGTGTATTAATGATGATG	358

QY 302 GGTGGGAGAGTGGCTGAGAACCTTACTACTAGCGTATGAGACCTCTGGGGCCAGAGGA 361
DB 359 GGGAGACTGACCTTT-----ACTACTACTACTACGGTATGACGCTCTGGGGCCAGAGGA 412
QY 362 CCACGGTACCGCTCTCTCA 381
DB 413 CCACGGTACCGCTCTCTCA 432

RESULT 2
US-09-240-274-95
; Sequence 95, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 95
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D31
US-09-240-274-95

Query Match 82.4%; Score 313.8; DB 3; Length 378;
Best Local Similarity 90.8%; Pred. No. 3.9e-90;
Matches 346; Conservative 0; Mismatches 32; Indels 3; Gaps 1;

QY 1 GAGGTGACAGCTGCTGAGTGTGGGGAGGCGCTGCTGACCTGGGAGGTCCCTGAGACTC 60
DB 1 GAGGTGACAGCTGCTGAGTGTGGGGAGGCGCTGCTGACCTGGGAGGTCCCTGAGACTC 60
QY 61 TCTGTGACAGCTGCTGAGTGTGGGGAGGCGCTGCTGACCTGGGAGGTCCCTGAGACTC 120
DB 61 TCTGTGACAGCTGCTGAGTGTGGGGAGGCGCTGCTGACCTGGGAGGTCCCTGAGACTC 120
QY 121 CCAGGCAAGGGGCTGAGTGTGGGGAGGCGCTGCTGACCTGGGAGGTCCCTGAGACTC 180
DB 121 CCAGGCAAGGGGCTGAGTGTGGGGAGGCGCTGCTGACCTGGGAGGTCCCTGAGACTC 180
QY 181 GAGAGCTCCGTGAAGGGGCGGATTCACATCTCCAGAGCAATTCAGAGCAACGCTGAT 240
DB 181 TGAAGCTCCGTGAAGGGGCGGATTCACATCTCCAGAGCAATTCAGAGCAACGCTGAT 240
QY 241 CTGCAATGAACAGCTGAGAGCTGAGAGCAAGGCGTGTATTATCTGTCGAAAGATATG 300
DB 241 CTGCAATGAACAGCTGAGAGCTGAGAGCAAGGCGTGTATTATCTGTCGAAAGATATG 300
QY 301 GGGTGGGAGTGGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCT 360
DB 301 AATTTTGGAGTGGT---ATTCCGCTACTACTACGGTATGAGAGTGTGGGGCCAGAGG 357
QY 361 ACCAGGTGACCGTCTCTCTCA 381
DB 358 ACCAGGTGACCGTCTCTCTCA 378

RESULT 3
US-09-240-274-94
; Sequence 94, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.

; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 94
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D30
US-09-240-274-94

Query Match 81.5%; Score 310.6; DB 3; Length 378;
Best Local Similarity 90.3%; Pred. No. 4.1e-89;
Matches 344; Conservative 0; Mismatches 34; Indels 3; Gaps 1;

QY 1 GAGGTGACAGCTGCTGAGTGTGGGGAGGCGCTGCTGACCTGGGAGGTCCCTGAGACTC 60
DB 1 GAGGTGACAGCTGCTGAGTGTGGGGAGGCGCTGCTGACCTGGGAGGTCCCTGAGACTC 60
QY 61 TCTGTGACAGCTGCTGAGTGTGGGGAGGCGCTGCTGACCTGGGAGGTCCCTGAGACTC 120
DB 61 TCTGTGACAGCTGCTGAGTGTGGGGAGGCGCTGCTGACCTGGGAGGTCCCTGAGACTC 120
QY 121 CCAGGCAAGGGGCTGAGTGTGGGGAGGCGCTGCTGACCTGGGAGGTCCCTGAGACTC 180
DB 121 CCAGGCAAGGGGCTGAGTGTGGGGAGGCGCTGCTGACCTGGGAGGTCCCTGAGACTC 180
QY 181 GAGAGCTCCGTGAAGGGGCGGATTCACATCTCCAGAGCAATTCAGAGCAACGCTGAT 240
DB 181 TGAAGCTCCGTGAAGGGGCGGATTCACATCTCCAGAGCAATTCAGAGCAACGCTGAT 240
QY 241 CTGCAATGAACAGCTGAGAGCTGAGAGCAAGGCGTGTATTATCTGTCGAAAGATATG 300
DB 241 CTGCAATGAACAGCTGAGAGCTGAGAGCAAGGCGTGTATTATCTGTCGAAAGATATG 300
QY 301 GGGTGGGAGTGGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCT 360
DB 301 AATTTTGGAGTGGT---ATTCCGCTACTACTACGGTATGAGAGTGTGGGGCCAGAGG 357
QY 361 ACCAGGTGACCGTCTCTCTCA 381
DB 358 ACCAGGTGACCGTCTCTCTCA 378

RESULT 4
US-09-240-274-196
; Sequence 196, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 196
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Homo sapiens

FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH56
US-09-424-274-196

Query Match
Best Local Similarity 81.5%; Score 310.6; DB 3; Length 378;
Pred. No. 4.1e-89;
Matches 344; Conservative 0; Mismatches 34; Indels 3; Gaps 1;

QY 1 GAGGTGACGCTGCTGAGTGTGGGGAGGCGCTGTCAGCTGGAGGTCCCTGAGACTC 60
DB 1 GAGGTGACGCTGCTGAGTGTGGGGAGGCGCTGTCAGCTGGAGGTCCCTGAGACTC 60
QY 61 TCCGTGACGCTGCTGAGTGTGGGGAGGCGCTGTCAGCTGGAGGTCCCTGAGACTC 120
DB 61 TCCGTGACGCTGCTGAGTGTGGGGAGGCGCTGTCAGCTGGAGGTCCCTGAGACTC 120
QY 121 CCAGGCAAGGGGCTGAGTGTGGGGAGGCGCTGTCAGCTGGAGGTCCCTGAGACTC 180
DB 121 CCAGGCAAGGGGCTGAGTGTGGGGAGGCGCTGTCAGCTGGAGGTCCCTGAGACTC 180
QY 181 GCGAGCTCCGTGAGAGGGCGGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTAT 240
DB 181 TCAGACTCCGTGAGAGGGCGGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTAT 240
QY 241 CTGCAATGAAACGCTGAGAGGCTGAGAGCAAGGCTGTGATTAATCTGCGAAAGATATG 300
DB 241 CTGCAATGAAACGCTGAGAGGCTGAGAGCAAGGCTGTGATTAATCTGCGAAAGATATG 300
QY 301 GGGTGGGAGGCTGAGAGGCTGAGAGCAAGGCTGTGATTAATCTGCGAAAGATATG 360
DB 301 GGGTGGGAGGCTGAGAGGCTGAGAGCAAGGCTGTGATTAATCTGCGAAAGATATG 360
QY 361 ACCAGGTCACCGCTCTCTCA 381
DB 358 ACCAGGTCACCGCTCTCTCA 378

RESULT 5
US-09-424-840-15
Sequence 15, Application US/09424840
Patent No. 6790938
GENERAL INFORMATION:
APPLICANT: BERCHTOLD, Peter
TITLE OF INVENTION: Anti-Grp78/70 Recombinant Antibodies
FILE REFERENCE: 100564-09049
CURRENT APPLICATION NUMBER: US/09/424,840
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: DE 19723904.8
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: DE 19820663.1
PRIOR FILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 127
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 372
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(372)
US-09-424-840-15

Query Match
Best Local Similarity 81.0%; Score 308.8; DB 4; Length 372;
Pred. No. 1.5e-88;
Matches 344; Conservative 0; Mismatches 27; Indels 9; Gaps 1;

QY 2 AGGTGACGCTGCTGAGTGTGGGGAGGCGCTGTCAGCTGGAGGTCCCTGAGACTC 61
DB 2 AGGTGACGCTGCTGAGTGTGGGGAGGCGCTGTCAGCTGGAGGTCCCTGAGACTC 61

QY 62 CCTGTGACGCTCTGAGTGTACCTTCAGTATGAGCACTGAGGTCCGCGAGGCTC 121
DB 62 CCTGTGACGCTCTGAGTGTACCTTCAGTATGAGCACTGAGGTCCGCGAGGCTC 121
QY 122 CAGGCAAGGGGCTGAGTGTGGGGAGGCGCTGTCAGCTGGAGGTCCCTGAGACTC 181
DB 122 CAGGCAAGGGGCTGAGTGTGGGGAGGCGCTGTCAGCTGGAGGTCCCTGAGACTC 181
QY 182 CAGACTCCGTGAGAGGGCGGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 241
DB 182 CAGACTCCGTGAGAGGGCGGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 241
QY 242 TCGAATGAAACGCTGAGAGGCTGAGAGCAAGGCTGTGATTAATCTGCGAAAGATATG 301
DB 242 TCGAATGAAACGCTGAGAGGCTGAGAGCAAGGCTGTGATTAATCTGCGAAAGATATG 301
QY 302 GGTGGGAGTGTGAGAGGCTGAGAGCAAGGCTGTGATTAATCTGCGAAAGATATG 361
DB 298 -----GGCGAGTGTGAGAGGCTGAGAGCAAGGCTGTGATTAATCTGCGAAAGATATG 352
QY 362 CCAAGGTCACCGCTCTCTCA 381
DB 353 CCAAGGTCACCGCTCTCTCA 372

RESULT 6
US-09-424-840-5
Sequence 5, Application US/09424840
Patent No. 6790938
GENERAL INFORMATION:
APPLICANT: BERCHTOLD, Peter
TITLE OF INVENTION: Anti-Grp78/70 Recombinant Antibodies
FILE REFERENCE: 100564-09049
CURRENT APPLICATION NUMBER: US/09/424,840
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: DE 19723904.8
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: DE 19820663.1
PRIOR FILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 127
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 369
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(369)
US-09-424-840-5

Query Match
Best Local Similarity 80.7%; Score 307.6; DB 4; Length 369;
Pred. No. 3.6e-88;
Matches 344; Conservative 0; Mismatches 24; Indels 12; Gaps 1;

QY 2 AGGTGACGCTGCTGAGTGTGGGGAGGCGCTGTCAGCTGGAGGTCCCTGAGACTC 61
DB 2 AGGTGACGCTGCTGAGTGTGGGGAGGCGCTGTCAGCTGGAGGTCCCTGAGACTC 61
QY 62 CCTGTGACGCTCTGAGTGTGGGGAGGCGCTGTCAGCTGGAGGTCCCTGAGACTC 121
DB 62 CCTGTGACGCTCTGAGTGTGGGGAGGCGCTGTCAGCTGGAGGTCCCTGAGACTC 121
QY 122 CAGGCAAGGGGCTGAGTGTGGGGAGGCGCTGTCAGCTGGAGGTCCCTGAGACTC 181
DB 122 CAGGCAAGGGGCTGAGTGTGGGGAGGCGCTGTCAGCTGGAGGTCCCTGAGACTC 181
QY 182 CAGACTCCGTGAGAGGGCGGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 241
DB 182 CAGACTCCGTGAGAGGGCGGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 241

QY 242 TGCAGATGAACAGCTGAGAGTGAAGACACGGCTGTGTATTAATCTGTGCGAAGATATG 301
DB 242 TGCAGATGAACAGCTGAGAGTGAAGACACGGCTGTGTATTAATCTGTGCGAAGATATG 301
QY 302 GGTGGGGAGCTGCTGAGAGACCTACTACTAGGTATGACGCTGGGGCCAAAGGA 361
DB 302 GGTGGGGAGCTGCTGAGAGACCTACTACTAGGTATGACGCTGGGGCCAAAGGA 349
QY 362 CCACGGTCAACCGTCTCTCA 381
DB 350 CCACGGTCAACCGTCTCTCA 369

RESULT 7
US-09-240-274-195

; Sequence 195, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 195
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-195

Query Match 79.8%; Score 304.2; DB 3; Length 378;
Best Local Similarity 89.2%; Pred. No. 4,4e-87;
Matches 340; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

QY 1 GAGGTGAGCTGCTGAGTCTGAGGGGAGGCTGCTGAGGCTGGAGGCTCCGAGATC 60
DB 1 GAGGTGAGCTGCTGAGTCTGAGGGGAGGCTGCTGAGGCTGGAGGCTCCGAGATC 60
QY 61 TCCGTGACAGCTGTGAGTTCACCTTCACTAGTATGAGCACTGGGTCGCCAGGCT 120
DB 61 TCCGTGACAGCTGTGAGTTCACCTTCACTAGTATGAGCACTGGGTCGCCAGGCT 120
QY 121 CCAGGCAAGGGCTGAGTGGGAGGCTATATCATATGATGAAAGTATAATATCTAT 180
DB 121 CCAGGCAAGGGCTGAGTGGGAGGCTATATCATATGATGAAAGTATAATATCTAT 180
QY 121 CTTGGCAAGGGCTGAGTGGGAGGCTATATGATGAAAGTATAATATCTAT 180
DB 121 CTTGGCAAGGGCTGAGTGGGAGGCTATATGATGAAAGTATAATATCTAT 180
QY 181 GCAGACTCCGTGAAGGCGCATTCACCATCTCCAGACAAATTCAGACGCTGTAT 240
DB 181 GCAGACTCCGTGAAGGCGCATTCACCATCTCCAGACAAATTCAGACGCTGTAT 240
QY 241 CTGCAATGAACAGCTGAGAGCTGAGACACGGCTGTGTATTAATCTGTGCGAAGATATG 300
DB 241 CTGCAATGAACAGCTGAGAGCTGAGACACGGCTGTGTATTAATCTGTGCGAAGATATG 300
QY 301 GGTGGGGAGCTGCTGAGAGACCTACTACTAGGTATGACGCTGGGGCCAAAGG 360
DB 301 GGTGGGGAGCTGCTGAGAGACCTACTACTAGGTATGACGCTGGGGCCAAAGG 357
QY 361 ACCAGGTCAACCGTCTCTCA 381
DB 358 ACCAGGTCAACCGTCTCTCA 378

RESULT 8
US-09-240-274-189

; Sequence 189, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 189
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH28, SH50, and SH53
US-09-240-274-189

Query Match 79.0%; Score 301; DB 3; Length 378;
Best Local Similarity 88.7%; Pred. No. 4.6e-86;
Matches 338; Conservative 0; Mismatches 40; Indels 3; Gaps 1;

QY 1 GAGGTGAGCTGCTGAGTCTGAGGGGAGGCTGCTGAGGCTGGAGGCTCCGAGATC 60
DB 1 GAGGTGAGCTGCTGAGTCTGAGGGGAGGCTGCTGAGGCTGGAGGCTCCGAGATC 60
QY 61 TCCGTGAGCTGCTGAGTTCACCTTCACTAGTATGAGCACTGGGTCGCCAGGCT 120
DB 61 TCCGTGAGCTGCTGAGTTCACCTTCACTAGTATGAGCACTGGGTCGCCAGGCT 120
QY 121 CCAGGCAAGGGCTGAGTGGGAGGCTATATCATATGATGAAAGTATAATATCTAT 180
DB 121 CCAGGCAAGGGCTGAGTGGGAGGCTATATCATATGATGAAAGTATAATATCTAT 180
QY 181 GCAGACTCCGTGAAGGCGCATTCACCATCTCCAGACAAATTCAGACGCTGTAT 240
DB 181 GCAGACTCCGTGAAGGCGCATTCACCATCTCCAGACAAATTCAGACGCTGTAT 240
QY 241 CTGCAATGAACAGCTGAGAGCTGAGACACGGCTGTGTATTAATCTGTGCGAAGATATG 300
DB 241 CTGCAATGAACAGCTGAGAGCTGAGACACGGCTGTGTATTAATCTGTGCGAAGATATG 300
QY 301 GGTGGGGAGCTGCTGAGAGACCTACTACTAGGTATGACGCTGGGGCCAAAGG 360
DB 301 GGTGGGGAGCTGCTGAGAGACCTACTACTAGGTATGACGCTGGGGCCAAAGG 357
QY 361 ACCAGGTCAACCGTCTCTCA 381
DB 358 ACCAGGTCAACCGTCTCTCA 378

RESULT 9
US-08-862-124-16

; Sequence 16, Application US/08862124
; Patent No. 6207153
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Maiti, Pradipt K.
; APPLICANT: Kaplan, Howard A.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT
; SPECIFICALLY DETECT CANCER CELLS, NICOTINOTIDES ENCODING THE
; FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
; TREATMENT OF CANCERS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Morrison & Foerster LLP
; STREET: 755 Page Mill Road
; CITY: Palo Alto

STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/862,124
FILING DATE: 22-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ. ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 867 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(1..855, 862..867)
US-08-862-124-16

Query Match 78.8%; Score 300.4; DB 3; Length 867;
Best Local Similarity 88.9%; Pred. No. 1e-85;
Matches 338; Conservative 0; Mismatches 36; Indels 6; Gaps 1;

QY 2 AGGTGAGCTGCTCGAGTCTGGGGAGGCGCTGGTCCAGCTGGAGGTCCCTGAGACTT 61
DB 428 AGGTGAGCTGCTGGAGTCTGGGGAGGCGCTGGTCCAGCTGGAGGTCCCTGAGACTT 487
QY 62 CCGTGCAGCTCTGTGATTACCTTCAGTAGTATGAGCATGACCTGGGTCCGCGAGGCTC 121
DB 488 CCGTGCAGCTCTGTGATTCCCTTCAGAACTTTGCTATGACCTGGGTCCGCGAGGCTC 547
QY 122 CAGGCAAGGGGCTGGAGTGGGTGAGTTATCATATGATGAGTAATTAATTAATCTATG 181
DB 548 TAGGCAAGGGGCTGGAGTGGGTGAGTTATCATATGATGAGTAATTAATTAATCTATG 607
QY 182 CAGACTCCGTTGAAGGGCCGATTACCATCTCCAGAGCAATTCAGAAACAGCGTGTATC 241
DB 608 CAGACTCCGTTGAAGGGCCGATTACCATCTCCAGAGCAATTCAGAAACAGCGTGTATC 667
QY 242 TGCATTAATGAACAGCTGAGAGCTGAGAGACAGCGCTGTGATTACTGTGCGAAAGATATG 301
DB 668 TAAATAATGAACAGCTGAGAGCTGAGAGACAGCGCTGTGATTACTGTGCGAGATCAAG 727
QY 302 GGTGGGGCAGTGGCTGAGAGACCTACTACTACGATATGACGTTCTGGGGCAGAGGGA 361
DB 728 GCGTGTGGGTGACT-----ATGACCACTACTACGATTTGAGCGTCTGGGGCAGAGGGA 781
QY 362 CCACGGTCAACCGTCTCTCTCA 381
DB 782 CCACGGTCAACCGTCTCTCTCA 801

RESULT 10
US-08-862-124-13
; Sequence 13, Application US/08862124
; Patent No. 6207153
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Maiti, Pradip K.
; APPLICANT: Kaplan, Howard A.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT

TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
; TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
; TITLE OF INVENTION: DETECTION OF CANCERS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster LLP
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/862,124
FILING DATE: 22-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ. ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(1..906, 913..918)
US-08-862-124-13

Query Match 78.8%; Score 300.4; DB 3; Length 918;
Best Local Similarity 88.9%; Pred. No. 1e-85;
Matches 338; Conservative 0; Mismatches 36; Indels 6; Gaps 1;

QY 2 AGGTGAGCTGCTCGAGTCTGGGGAGGCGCTGGTCCAGCTGGAGGTCCCTGAGACTT 61
DB 479 AGGTGAGCTGCTGGAGTCTGGGGAGGCGCTGGTCCAGCTGGAGGTCCCTGAGACTT 538
QY 62 CCGTGCAGCTCTGTGATTACCTTCAGTAGTATGAGCATGACCTGGGTCCGCGAGGCTC 121
DB 539 CCGTGCAGCTCTGTGATTCCCTTCAGAACTTTGCTATGACCTGGGTCCGCGAGGCTC 598
QY 122 CAGGCAAGGGGCTGGAGTGGGTGAGTTATCATATGATGAGTAATTAATTAATCTATG 181
DB 599 TAGGCAAGGGGCTGGAGTGGGTGAGTTATCATATGATGAGTAATTAATTAATCTATG 658
QY 182 CAGACTCCGTTGAAGGGCCGATTACCATCTCCAGAGCAATTCAGAAACAGCGTGTATC 241
DB 659 CAGACTCCGTTGAAGGGCCGATTACCATCTCCAGAGCAATTCAGAAACAGCGTGTATC 718
QY 242 TGCATTAATGAACAGCTGAGAGCTGAGAGACAGCGCTGTGATTACTGTGCGAAAGATATG 301
DB 719 TAAATAATGAACAGCTGAGAGCTGAGAGACAGCGCTGTGATTACTGTGCGAGATCAAG 778
QY 302 GGTGGGGCAGTGGCTGAGAGACCTACTACTACGATATGACGTTCTGGGGCAGAGGGA 361
DB 779 GCGTGTGGGTGACT-----ATGACCACTACTACGATTTGAGCGTCTGGGGCAGAGGGA 832
QY 362 CCACGGTCAACCGTCTCTCTCA 381
DB 833 CCACGGTCAACCGTCTCTCTCA 852

RESULT 11

US-08-862-124-15/c
; Sequence 15, Application US/08862124
; Patent No. 6207153
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Maiti, Pradip K.
; APPLICANT: Kaplan, Howard A.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT
; TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
; TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
; TITLE OF INVENTION: DETECTION OF CANCERS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster LLP
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,124
; FILING DATE: 22-MAY-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 31608-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 918 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-862-124-15
Query Match 78.8%; Score 300.4; DB 3; Length 918;
Best Local Similarity 88.9%; Pred. No. 1.1e-85;
Matches 338; Conservative 0; Mismatches 36; Indels 6; Gaps 1;
Db 2 AGGTGACGCTGCTGAGTCTGGGGAGAGCGCTGCTGACGCTGGAGAGTCCCTGAGACTCT 61
440 AGGTGACGCTGCTGAGTCTGGGGAGAGCGCTGCTGACGCTGGAGAGTCCCTGAGACTCT 381
QY 62 CCTGTGACGCTCTGATTCACCTTCAGTACGATGAGCATGCACTGGGTCCGCAAGCTC 121
Db 380 CCGTGTGACGCTCTGATTCACCTTCAGTACGATGAGCATGCACTGGGTCCGCAAGCTC 321
QY 122 CAGGCAAGGGGCTGAGTGGTGGCACTTATCATATGATGAGAGTAATAATACATG 181
Db 320 TAGGCAAGGGGCTGAGTGGTGGCACTTATCATATGATGAGAGTAATAATACATG 261
QY 182 CAGACTCCGTGAGAGGGCCGATTCACATCTCCAGAGCAATTCAGAGAACACCGCTGATC 241
Db 260 CAGACTCCGTGAGAGGGCCGATTCACATCTCCAGAGCAATTCAGAGAACACCGCTGATC 201
QY 242 TGAATATGAAAGCTTGAAGCTGAGAGCAACGCTGTGTATTAATGTCGAAAGATATG 301
Db 200 TGAATATGAAAGCTTGAAGCTGAGAGCAACGCTGTGTATTAATGTCGAAAGATATG 141
QY 302 GGTGGGGCAGTGGTGGAGACCCCTACTACTAGGATGAGAGCGTGGGGCCAAAGGA 361
Db 140 GCTGTGTGGTGACT-----ATGACCACTACTAGGATGAGAGCGTGGGGCCAAAGGA 87
QY 362 CCACGGTACCGCTCTCTCA 381

Db 86 CCACGGTACCGCTCTCTCA 67
RESULT 12
US-09-560-198A-1
; Sequence 1, Application US/09560198A
; Patent No. 6492497
; GENERAL INFORMATION:
; APPLICANT: Thompson, Julia E
; APPLICANT: Leonard, Simon N
; APPLICANT: Wilton, Alison J
; APPLICANT: Braddock, Peter SH
; APPLICANT: Du Fou, Sarah L
; APPLICANT: McCafferty, John G
; APPLICANT: Conroy, Louise A
; TITLE OF INVENTION: Specific binding members for TGFbeta1
; FILE REFERENCE: 2811/35620A
; CURRENT APPLICATION NUMBER: US/09/560,198A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/131,983
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-560-198A-1
Query Match 78.6%; Score 299.6; DB 4; Length 369;
Best Local Similarity 89.2%; Pred. No. 1.3e-85;
Matches 339; Conservative 0; Mismatches 29; Indels 12; Gaps 1;
Db 2 AGGTGACGCTGCTGAGTCTGGGGAGAGCGCTGCTGACGCTGGAGAGTCCCTGAGACTCT 61
2 AGGTGACGCTGCTGAGTCTGGGGAGAGCGCTGCTGACGCTGGAGAGTCCCTGAGACTCT 61
QY 62 CCTGTGACGCTCTGATTCACCTTCAGTACGATGAGCATGCACTGGGTCCGCAAGCTC 121
Db 62 CCGTGTGACGCTCTGATTCACCTTCAGTACGATGAGCATGCACTGGGTCCGCAAGCTC 121
QY 122 CAGGCAAGGGGCTGAGTGGTGGCACTTATCATATGATGAGAGTAATAATACATG 181
Db 122 CAGGCAAGGGGCTGAGTGGTGGCACTTATCATATGATGAGAGTAATAATACATG 181
QY 182 CAGACTCCGTGAGAGGGCCGATTCACATCTCCAGAGCAATTCAGAGAACACCGCTGATC 241
Db 182 CAGACTCCGTGAGAGGGCCGATTCACATCTCCAGAGCAATTCAGAGAACACCGCTGATC 241
QY 242 TGAATATGAAAGCTTGAAGCTGAGAGCAACGCTGTGTATTAATGTCGAAAGATATG 301
Db 242 TGAATATGAAAGCTTGAAGCTGAGAGCAACGCTGTGTATTAATGTCGAAAGATATG 297
QY 302 GGTGGGGCAGTGGTGGAGACCCCTACTACTAGGATGAGAGCGTGGGGCCAAAGGA 361
Db 298 -----GTTGATATATAGTGGCTGAGATGAGAGCGTGGGGCCAAAGGA 349
QY 362 CCACGGTACCGCTCTCTCA 381
Db 350 CCACGGTACCGCTCTCTCA 369

RESULT-13
US-09-240-274-87
; Sequence 87, Application US/09240274
; Patent No. 6253455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rb(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202

CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 87
LENGTH: 381
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain D13
US-09-240-274-87

Query Match 78.6%; Score 299.4; DB 3; Length 381;
Best Local Similarity 86.6%; Pred. No. 1.5e-85;
Matches 330; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 GAGGTGACACTGCTGAGTCTGGGGAGGCGCTGTCAGGCTGGAGGTCCTGAGACTC 60
DB 1 GAGGTGACACTGCTGAGTCTGGGGAGGCGCTGTCAGGCTGGAGGTCCTGAGACTC 60
QY 61 TCTGTGACAGCGCTGAGTTCACCTTCAGTACTATGAGTGGATGCACTGGGCGCGAGGCT 120
DB 61 TCTGTGACAGCGCTGAGTTCACCTTCAGTACTATGAGTGGATGCACTGGGCGCGAGGCT 120
QY 121 CCAGGCAAGGGGCTGAGTGGTGGAGTATATCATATGATGAAGTAAATAACTAT 180
DB 121 CCAGGCAAGGGGCTGAGTGGTGGAGTATATGATGAAGTAAATAACTAT 180
QY 181 GCAGACTCCGTGAGAGGCGGATTCACCATCTCCAGAGACATTCAGAAACAGCTGTAT 240
DB 181 GCAGACTCCGTGAGAGGCGGATTCACCATCTCCAGAGACATTCAGAAACAGCTGTAT 240
QY 241 CTGCAATGAAAGCGCTGAGGCTGAGAGACAGGCGTGTATCTAGCTGGGAAAGATATG 300
DB 241 CTGCAATGAAAGCGCTGAGGCTGAGAGACAGGCGTGTATCTAGCTGGGAAAGATATG 300
QY 301 GGGTGGGGGAGTGGCTGAGAGACCTTACTACTAGCGTATGAGCGTGGGGCCAGAGG 360
DB 301 GGGTGGGGGAGTGGCTGAGAGACCTTACTACTAGCGTATGAGCGTGGGGCCAGAGG 360
QY 361 ACCAGGTGACCGCTCTCTCA 381.
DB 361 ACCAGGTGACCGCTCTCTCA 381

RESULT 14
US-08-862-124-18/c
Sequence 18, Application US/08862124
Patent No. 6207153
GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
APPLICANT: Maiti, Pradip K.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/862,124
FILING DATE: 22-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 867 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-862-124-18

Query Match 78.4%; Score 298.8; DB 3; Length 867;
Best Local Similarity 88.7%; Pred. No. 3.3e-85;
Matches 337; Conservative 0; Mismatches 37; Indels 6; Gaps 1;

QY 2 AGGTGAGCTGCTGAGTCTGGGGAGGCGCTGTCAGGCTGGAGGTCCTGAGACTCT 61
DB 440 AGGTGAGCTGCTGAGTCTGGGGAGGCGCTGTCAGGCTGGAGGTCCTGAGACTCT 381
QY 62 CCTGTGACAGCGCTGAGTTCACCTTCAGTACTATGAGTGGATGCACTGGGCGCGAGGCT 121
DB 380 CCTGTGACAGCGCTGAGTTCACCTTCAGTACTATGAGTGGATGCACTGGGCGCGAGGCT 321
QY 122 CAGGCAAGGGGCTGAGTGGTGGAGTATATCATATGATGAAGTAAATAACTATG 181
DB 320 TAGGCAAGGGGCTGAGTGGTGGAGTATATCATATGATGAAGTAAATAACTATG 261
QY 182 CAGACTCCGTGAGAGGCGGATTCACCATCTCCAGAGACATTCAGAAACAGCTGTAT 241
DB 260 CAGACTCCGTGAGAGGCGGATTCACCATCTCCAGAGACATTCAGAAACAGCTGTAT 201
QY 242 TGAATGAAAGCGCTGAGGCTGAGAGACAGGCGTGTATCTAGCTGGGAAAGATATG 301
DB 200 TGAATGAAAGCGCTGAGGCTGAGAGACAGGCGTGTATCTAGCTGGGAAAGATATG 141
QY 302 GGTGGGGAGTGGCTGAGAGACCTTACTACTAGCGTATGAGCGTGGGGCCAGAGG 361
DB 140 GCTGTGGGTACT-----ATGACACTACTAGCGTTGTGTCGTGGGGCAAGAGG 87
QY 362 CCAGGTGACCGCTCTCTCA 381
DB 86 CCAGGTGACCGCTCTCTCA 67

RESULT 15
US-09-240-274-86
Sequence 86, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 86
LENGTH: 378

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh (D) chain D12
US-09-240-274-86

Query Match 78.2%; Score 297.8; DB 3; Length 378;
Best Local Similarity 88.2%; Pred. No. 4.8e-85;
Matches 336; Conservative 0; Mismatches 42; Indels 3; Gaps 1;

```
QY 1 GAGGTCCAGCTGCTGAGTCTGAGGAGGCTGCTCAGCTGGGAGGTCCCTGAGACTC 60
    |||
Db 1 GAGGTCCAGCTGCTGAGTCTGAGGAGGCTGCTCAGCTGGGAGGTCCCTGAGACTC 60
    |||
QY 61 TCCTGTGACAGCCTCTGATTTCACTTCAGTAGCTATGAGCATGCACTGGGTCCGAGGCT 120
    |||
Db 61 GCCTGTGACAGCCTCTGATTTCACTTCAGTAGCTATGAGCATGCACTGGGTCCGAGGCT 120
    |||
QY 121 CCAGGCAAGGGGCTGAGTGGGTGAGCAATTATCATATGATGAAAGTAAATATCTAT 180
    |||
Db 121 CCAGGCAAGGGGCTGAGTGGGTGAGCAATTATCATATGATGAAAGTAAATATCTAT 180
    |||
QY 181 GCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACAGCTGTAT 240
    |||
Db 181 GTAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACAGCTGTAT 240
    |||
QY 241 CTGCAATGAAACAGCCTGAGAGCTGAGAACACGCGTGTGTATTTACTGTGCGAAAGATATG 300
    |||
Db 241 CTGGAATGAAACAGCCTGAGAGCTGAGAACACGCGTGTGTATTTACTGTGCGAGAGA--G 297
    |||
QY 301 GGGTGGGGCAGTGGCTGAGAACCTTACTACTACTAGGTATGAGCGTGGGGCCAGGG 360
    |||
Db 298 GCGTCTATGCTTGGCGGAATTAGCAAGTACTACTACGCGATGAGCGTGTGGGGCCAGGG 357
    |||
QY 361 ACCACGGTCACCGTCTCTCA 381
    |||
Db 358 ACCACGGTCACCGTCTCTCA 378
    |||
```

Search completed: December 7, 2004, 08:57:55
Job time : 79.6581 secs

Db 121 CCAGGCAAGGGGCTGAGTGGGAGGCTGATATATCATATGATGAAGTAAATATCTAT 180
181 GCAGACTCCGTGAGAGGGCCGATTCCACCATCTCCAGAGACAATTCAGAACACGCTGTAT 240
Db 181 GCAGACTCCGTGAGAGGGCCGATTCCACCATCTCCAGAGACAATTCAGAACACGCTGTAT 240
QY 241 CTGCAATATGAACGCTGAGAGCTGAGAGACACGGCTGTATTAATCTGTGGAAGATATG 300
Db 241 CTGCAATATGAACGCTGAGAGCTGAGAGACACGGCTGTATTAATCTGTGGAAGATATG 300
QY 301 GGGTGGGGGAGTGGCTGAGAGACCTTACTACTAGATGAGACGCTTGGGGCCAAGG 360
Db 301 GGGTGGGGGAGTGGCTGAGAGACCTTACTACTAGATGAGACGCTTGGGGCCAAGG 360
QY 361 ACCACGGTCAACCGTCTCTCA 381
Db 361 ACCACGGTCAACCGTCTCTCA 381

RESULT 2

US-10-309-762-211
; Sequence 211, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Guddas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Honda, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 211
; LENGTH: 379
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-762-211

Query Match 85.5%; Score 325.6; DB 16; Length 379;
Best Local Similarity 92.9%; Pred. No. 2.3e-95;
Matches 353; Conservative 0; Mismatches 24; Indels 3; Gaps 1;

QY 2 AGGTGACGCTGCTGAGTCTGGGGGAGGCGCTGGTCCAGCCTGGAGAGTCCCTGAGACTCT 61
Db 2 AGGTGACGCTGCTGAGTCTGGGGGAGGCGCTGGTCCAGCCTGGAGAGTCCCTGAGACTCT 61
QY 62 CCTGTGACGCTCTGGATTCACTTCACTAGTATGAGCATGACATGGGTCGCCCAAGCTC 121
Db 62 CCTGTGACGCTCTGGATTCACTTCACTAGTATGAGCATGACATGGGTCGCCCAAGCTC 121
QY 122 CAGGCAAGGGGCTGAGTGGGCTGAGTATATCATATATGAAGTAAATATCTATG 181
Db 122 CAGGCAAGGGGCTGAGTGGGCTGAGTATATCATATATGAAGTAAATATCTATG 181
QY 182 CAGACTCCGTGAGAGGGCCGATTCCACCATCTCCAGAGACAATTCAGAACACGCTGTATC 241
Db 182 CAGACTCCGTGAGAGGGCCGATTCCACCATCTCCAGAGACAATTCAGAACACGCTGTATC 241
QY 242 TGCATATGAACAGCTGAGAGCTGAGAGACAGGCTGTGTATTAATCTGTGGAAGATATG 301
Db 242 TGCATATGAACAGCTGAGAGCTGAGAGACAGGCTGTGTATTAATCTGTGGAAGATATG 301
QY 302 GGTGGGGGAGTGGCTGAGAGACCTTACTACTAGATGAGACGCTTGGGGCCAAGGA 361
Db 302 GGTGGGGGAGTGGCTGAGAGACCTTACTACTAGATGAGACGCTTGGGGCCAAGGA 361
QY 362 CCACGGTCAACCGTCTCTCA 381
Db 362 CCACGGTCAACCGTCTCTCA 381

Db 359 CCACGGTCAACCGTCTCTCA 378

RESULT 3

US-10-153-382-16
; Sequence 16, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PRIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC2019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 1413
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-153-382-16

Query Match 85.1%; Score 324.4; DB 14; Length 1413;
Best Local Similarity 92.9%; Pred. No. 8.4e-95;
Matches 353; Conservative 0; Mismatches 21; Indels 6; Gaps 1;

QY 2 AGGTGACGCTGCTGAGTCTGGGGGAGGCGCTGGTCCAGCCTGGAGAGTCCCTGAGACTCT 61
Db 59 AGGTGACGCTGCTGAGTCTGGGGGAGGCGCTGGTCCAGCCTGGAGAGTCCCTGAGACTCT 118
QY 62 CCTGTGACGCTCTGGATTCACTTCACTAGTATGAGCATGACATGGGTCGCCCAAGCTC 121
Db 119 CCTGTGACGCTCTGGATTCACTTCACTAGTATGAGCATGACATGGGTCGCCCAAGCTC 178
QY 122 CAGGCAAGGGGCTGAGTGGGCTGAGTATATCATATATGAAGTAAATATCTATG 181
Db 179 CAGGCAAGGGGCTGAGTGGGCTGAGTATATCATATATGAAGTAAATATCTATG 238
QY 182 CAGACTCCGTGAGAGGGCCGATTCCACCATCTCCAGAGACAATTCAGAACACGCTGTATC 241
Db 239 CAGACTCCGTGAGAGGGCCGATTCCACCATCTCCAGAGACAATTCAGAACACGCTGTATC 298
QY 242 TGCATATGAACAGCTGAGAGCTGAGAGACAGGCTGTGTATTAATCTGTGGAAGATATG 301
Db 299 TGCATATGAACAGCTGAGAGCTGAGAGACAGGCTGTGTATTAATCTGTGGAAGATATG 358
QY 302 GGTGGGGGAGTGGCTGAGAGACCTTACTACTAGATGAGACGCTTGGGGCCAAGGA 361
Db 359 GGTGGGGGAGTGGCTGAGAGACCTTACTACTAGATGAGACGCTTGGGGCCAAGGA 412
QY 362 CCACGGTCAACCGTCTCTCA 381
Db 413 CCACGGTCAACCGTCTCTCA 432

RESULT 4
US-10-612-497-61
; Sequence 61, Application US/10612497
; Publication No. US20040228858A1
; GENERAL INFORMATION:
; APPLICANT: Douglas C. Hanson
; APPLICANT: Mark J. Neveu
; APPLICANT: Eileen B. Mueller
; APPLICANT: Jeffrey H. Hanke
; APPLICANT: Steven C. Gilman
; APPLICANT: C. Geoffrey Davis
; APPLICANT: Jose R. Corvalan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PP1 DIV1
; CURRENT APPLICATION NUMBER: US/10/612,497
; CURRENT FILING DATE: 2003-07-01

```

; PRIOR APPLICATION NUMBER: US 09/472087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 61
; LENGTH: 1413
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-612-497-61

Query Match      85.1%; Score 324.4; DB 18; Length 1413;
Best Local Similarity 92.9%; Pred. No. 8.4e-95;
Matches 353; Conservative 0; Mismatches 21; Indels 6; Gaps 1;

QY 2 AGGTGACGCTGCTGAGTCTGGGGGAGGCGTGGTCCAGGCTGGAGAGTCCCTGAGACTCT 61
DB 59 AGGTGACGCTGCTGAGTCTGGGGGAGGCGTGGTCCAGGCTGGAGAGTCCCTGAGACTCT 118
QY 62 CCTGTGACGCTCTGTGATTCACTTCACTAGTATGAGATGCACTGGGTCGCGCAGGCTC 121
DB 119 CCTGTGACGCTCTGTGATTCACTTCACTAGTATGAGATGCACTGGGTCGCGCAGGCTC 178
QY 122 CAGGCAAGGGGCTGGAGTGGGTGGGCTGATTAATGATGAGATTAATAATCTATG 181
DB 179 CAGGCAAGGGGCTGGAGTGGGTGGGCTGATTAATGATGAGATTAATAATCTATG 238
QY 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCCAGAAACAGCTGTATC 241
DB 239 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCCAGAAACAGCTGTATC 298
QY 242 TGCATAATGAACAGCTGAGAGCTGAGAGACAGGCTGTGATTACTGTGCGAAAGATATG 301
DB 299 TGCATAATGAACAGCTGAGAGCTGAGAGACAGGCTGTGATTACTGTGCGAAAGATATG 358
QY 302 GGTGGGGAGTGGCTGGAGACCTTACTACTACGCTATGACGCTGTGGGCGCAAGGGA 361
DB 359 GGTGGGGAGTGGCTGGAGACCTTACTACTACGCTATGACGCTGTGGGCGCAAGGGA 412
QY 362 CCACGGTCAACGCTCTCTCTCA 381
DB 413 CCACGGTCAACGCTCTCTCTCA 432

RESULT 5
US-10-776-649-61
; Sequence 61, Application US/10776649
; Publication No. US2004022861A1
; GENERAL INFORMATION:
; APPLICANT: Douglas C. Hanson
; APPLICANT: Mark J. Neveu
; APPLICANT: Eileen E. Mueller
; APPLICANT: Jeffrey H. Hanke
; APPLICANT: Steven C. Gilman
; APPLICANT: C. Geoffrey Davis
; APPLICANT: Jose R. Corvalan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI DIV2
; CURRENT APPLICATION NUMBER: US/10/776,649
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 10/612497
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 09/472087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 61
; LENGTH: 1413
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```

US-10-776-649-61

Query Match      85.1%; Score 324.4; DB 18; Length 1413;
Best Local Similarity 92.9%; Pred. No. 8.4e-95;
Matches 353; Conservative 0; Mismatches 21; Indels 6; Gaps 1;

QY 2 AGGTGACGCTGCTGAGTCTGGGGGAGGCGTGGTCCAGGCTGGAGAGTCCCTGAGACTCT 61
DB 59 AGGTGACGCTGCTGAGTCTGGGGGAGGCGTGGTCCAGGCTGGAGAGTCCCTGAGACTCT 118
QY 62 CCTGTGACGCTCTGTGATTCACTTCACTAGTATGAGATGCACTGGGTCGCGCAGGCTC 121
DB 119 CCTGTGACGCTCTGTGATTCACTTCACTAGTATGAGATGCACTGGGTCGCGCAGGCTC 178
QY 122 CAGGCAAGGGGCTGGAGTGGGTGGGCTGATTAATGATGAGATTAATAATCTATG 181
DB 179 CAGGCAAGGGGCTGGAGTGGGTGGGCTGATTAATGATGAGATTAATAATCTATG 238
QY 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCCAGAAACAGCTGTATC 241
DB 239 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCCAGAAACAGCTGTATC 298
QY 242 TGCATAATGAACAGCTGAGAGCTGAGAGACAGGCTGTGATTACTGTGCGAAAGATATG 301
DB 299 TGCATAATGAACAGCTGAGAGCTGAGAGACAGGCTGTGATTACTGTGCGAAAGATATG 358
QY 302 GGTGGGGAGTGGCTGGAGACCTTACTACTACGCTATGACGCTGTGGGCGCAAGGGA 361
DB 359 GGTGGGGAGTGGCTGGAGACCTTACTACTACGCTATGACGCTGTGGGCGCAAGGGA 412
QY 362 CCACGGTCAACGCTCTCTCTCA 381
DB 413 CCACGGTCAACGCTCTCTCTCA 432

RESULT 6
US-10-041-860-75
; Sequence 75, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezebe, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGF AND USES
; FILE REFERENCE: ABGENIX-051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 75
; LENGTH: 382
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-041-860-75

Query Match      85.0%; Score 324; DB 15; Length 382;
Best Local Similarity 90.8%; Pred. No. 7.5e-95;
Matches 345; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 2 AGGTGACGCTGCTGAGTCTGGGGGAGGCGTGGTCCAGGCTGGAGAGTCCCTGAGACTCT 61
DB 2 AGGTGACGCTGCTGAGTCTGGGGGAGGCGTGGTCCAGGCTGGAGAGTCCCTGAGACTCT 61
QY 62 CCTGTGACGCTCTGTGATTCACTTCACTAGTATGAGATGCACTGGGTCGCGCAGGCTC 121
DB 62 CCTGTGACGCTCTGTGATTCACTTCACTAGTATGAGATGCACTGGGTCGCGCAGGCTC 121
```

QY 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTATATCATATATGAGATTAATAATCTATG 181
DB 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTATATATGATATGAGATTAATAATCTATG 181
QY 182 CAGACTCCCGTGAAGGGCCGCTTACCGCTCCAGAGACAAATTCAGAAACAGCGTGTATC 241
DB 182 CAGACTCCCGTGAAGGGCCGCTTACCGCTCCAGAGACAAATTCAGAAACAGCGTGTATC 241
QY 242 TGCAGATGAACAGCTGAGAGTGAAGACACGGCTGTATTAATCTGTGCGAAAGATATG 301
DB 242 TGCAGATGAACAGCTGAGAGTGAAGACACGGCTGTATTAATCTGTGCGAGAGATATG 301
QY 302 GGTGGGGCAGTGGCTGAGACCTTACTACTACTAGCGTATGACGCTGTGGGCGCAAGGGA 361
DB 302 ACTATATATGATGATGATTAATCTTACTACTACTAGCGTATGACGCTGTGGGCGCAAGGGA 361
QY 362 CCACGGTCAACCGCTCTCTCA 381
DB 362 CCACGGTCAACCGCTCTCTCA 381

RESULT 7

US-10-665-383-45
; Sequence 45, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Keyt, Bruce
; APPLICANT: Gazit, Gad
; APPLICANT: LaRoche, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; FILE REFERENCE: ABENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/411,137
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 382
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-665-383-45

Query Match 85.0%; Score 324; DB 17; Length 382;
Best Local Similarity 90.8%; Pred. No. 7.5e-95;
Matches 345; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY 2 AGGTGACGCTGCTGAGATCTGGGGGAGGCGTGTCCAGCTGGGAGGTCCCTGAGACTCT 61
DB 2 AGGTGACGCTGCTGAGATCTGGGGGAGGCGTGTCCAGCTGGGAGGTCCCTGAGACTCT 61
QY 62 CCTGTGACGCTCTGAGATTCACCTTCACTAGTATGAGCATGACACTGGGTCCGCAAGGCTC 121
DB 62 CCTGTGACGCTCTGAGATTCACCTTCACTAGTATGAGCATGACACTGGGTCCGCAAGGCTC 121
QY 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTATATCATATGAGAGATTAATAATCTATG 181
DB 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTATATATGATGAGAGATTAATAATCTATG 181
QY 182 CAGACTCCCGTGAAGGGCCGCTTACCGCTCCAGAGACAAATTCAGAAACAGCGTGTATC 241
DB 182 CAGACTCCCGTGAAGGGCCGCTTACCGCTCCAGAGACAAATTCAGAAACAGCGTGTATC 241
QY 242 TGCAGATGAACAGCTGAGAGTGAAGACACGGCTGTATTAATCTGTGCGAAAGATATG 301
DB 242 TGCAGATGAACAGCTGAGAGTGAAGACACGGCTGTATTAATCTGTGCGAGAGATATG 301
QY 302 GGTGGGGCAGTGGCTGAGACCTTACTACTACTAGCGTATGACGCTGTGGGCGCAAGGGA 361
DB 302 ACTATATATGATGATGATTAATCTTACTACTACTAGCGTATGACGCTGTGGGCGCAAGGGA 361

QY 362 CCACGGTCAACCGCTCTCTCA 381
DB 362 CCACGGTCAACCGCTCTCTCA 381

RESULT 8

US-10-041-860-67
; Sequence 67, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gad
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
; FILE REFERENCE: ABENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 379
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-041-860-67

Query Match 84.6%; Score 322.4; DB 15; Length 379;
Best Local Similarity 92.4%; Pred. No. 2.5e-94;
Matches 351; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

QY 2 AGGTGACGCTGCTGAGATCTGGGGGAGGCGTGTCCAGCTGGGAGGTCCCTGAGACTCT 61
DB 2 AGGTGACGCTGCTGAGATCTGGGGGAGGCGTGTCCAGCTGGGAGGTCCCTGAGACTCT 61
QY 62 CCTGTGACGCTCTGAGATTCACCTTCACTAGTATGAGCATGACACTGGGTCCGCAAGGCTC 121
DB 62 CCTGTGACGCTCTGAGATTCACCTTCACTAGTATGAGCATGACACTGGGTCCGCAAGGCTC 121
QY 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTATATCATATGAGAGATTAATAATCTATG 181
DB 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTATATGATGAGAGATTAATAATCTATG 181
QY 182 CAGACTCCCGTGAAGGGCCGCTTACCGCTCCAGAGACAAATTCAGAAACAGCGTGTATC 241
DB 182 CAGACTCCCGTGAAGGGCCGCTTACCGCTCCAGAGACAAATTCAGAAACAGCGTGTATC 241
QY 242 TGCAGATGAACAGCTGAGAGTGAAGACACGGCTGTATTAATCTGTGCGAAAGATATG 301
DB 242 TGCAGATGAACAGCTGAGAGTGAAGACACGGCTGTATTAATCTGTGCGAGAGATATG 301
QY 302 GGTGGGGCAGTGGCTGAGACCTTACTACTACTAGCGTATGACGCTGTGGGCGCAAGGGA 361
DB 302 GATTAAGCTATGTT--ACGCTTACTAGACTAGGATGAGAGCTGTGGGCGCAAGGGA 358
QY 362 CCACGGTCAACCGCTCTCTCA 381
DB 359 CCACGGTCAACCGCTCTCTCA 378

RESULT 9

US-10-665-383-29
; Sequence 29, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Keyt, Bruce
; APPLICANT: Gazit, Gad

```

; APPLICANT: LaRoche, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
; FILE REFERENCE: ABGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; PRIOR FILING DATE: 2003-09-16
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 379
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-665-383-29

Query Match      84.6%; Score 322.4; DB 17; Length 379;
Best Local Similarity 92.4%; Pred. No. 2.5e-94;
Matches 351; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

QY      2 AGGTGACGCTGCTCGAGTCTGGGGAGGCGCTGCTCCAGCTGGAGAGTCCCTGAGACTCT 61
DB      2 AGGTGACGCTGGTGGAGTCTGGGGAGGCGGTGCTCCAGCTGGAGAGTCCCTGAGACTCT 61

QY      62 CCTGTGACGCTCTGGATTCACTTCACTAGTATGAGTGCAGTGGGTCCCGCAGGCTC 121
DB      62 CCTGTGACGCTCTGGATTCACTTCACTAGTATGAGTGCAGTGGGTCCCGCAGGCTC 121

QY      122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGGAATTAATAATACTATG 181
DB      122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATGATGATGGAATTAATAATACTATG 181

QY      182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGAACAGCGCTGATC 241
DB      182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGAACAGCGCTGATC 241

QY      242 TGCATATGAACAGCTGAGAGCTGAGAGCAACGCGCTGTGATTAATCTGTGGAAGATATG 301
DB      242 TGCATATGAACAGCTGAGAGCTGAGAGCAACGCGCTGTGATTAATCTGTGGAAGATATG 301

QY      302 GGTGGGGCAGTGGCTGAGAGCCCTACTACTACTAGGTAATGAGCGTCTGGGGCAGAGGA 361
DB      302 GATTAACGCTATGCTT---ACGCTTACTACTAGGTAATGAGCGTCTGGGGCAGAGGA 358

QY      362 CCACGGTCAACGCTCTCTCTCA 381
DB      359 CCACGGTCAACGCTCTCTCTCA 378

RESULT 10
US-10-309-762-207
; Sequence 207, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Guddar, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 382
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-762-207
```

```

Query Match      84.6%; Score 322.4; DB 16; Length 382;
Best Local Similarity 90.5%; Pred. No. 2.5e-94;
Matches 344; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY      2 AGGTGACGCTGCTCGAGTCTGGGGAGGCGCTGCTCCAGCTGGAGAGTCCCTGAGACTCT 61
DB      2 AGGTGACGCTGGTGGAGTCTGGGGAGGCGGTGCTCCAGCTGGAGAGTCCCTGAGACTCT 61

QY      62 CCTGTGACGCTCTGGATTCACTTCACTAGTATGAGTGCAGTGGGTCCCGCAGGCTC 121
DB      62 CCTGTGACGCTCTGGATTCACTTCACTAGTATGAGTGCAGTGGGTCCCGCAGGCTC 121

QY      122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGGAATTAATAATACTATG 181
DB      122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATGATGGAATTAATAATACTATG 181

QY      182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGAACAGCGCTGATC 241
DB      182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGAACAGCGCTGATC 241

QY      242 TGCATATGAACAGCTGAGAGCTGAGAGCAACGCGCTGTGATTAATCTGTGGAAGATATG 301
DB      242 TGCATATGAACAGCTGAGAGCTGAGAGCAACGCGCTGTGATTAATCTGTGGAAGATATG 301

QY      302 GGTGGGGCAGTGGCTGAGAGCCCTACTACTACTAGGTAATGAGCGTCTGGGGCAGAGGA 361
DB      302 GATTACTATGTTCTGGGGAGTTATCCCACTAGGTAATGAGCGTCTGGGGCAGAGGA 361

QY      362 CCACGGTCAACGCTCTCTCTCA 381
DB      362 CCACGGTCAACGCTCTCTCTCA 381

RESULT 11
US-10-269-711-42
; Sequence 42, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Devries, Peter J.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Ostrow, Dave
; APPLICANT: Weller, James
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 6989 US 01
; CURRENT APPLICATION NUMBER: US/10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 370
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-269-711-42

Query Match      84.5%; Score 322; DB 16; Length 370;
Best Local Similarity 92.9%; Pred. No. 3.3e-94;
Matches 353; Conservative 0; Mismatches 15; Indels 12; Gaps 1;

QY      2 AGGTGACGCTGCTCGAGTCTGGGGAGGCGCTGCTCCAGCTGGAGAGTCCCTGAGACTCT 61
DB      2 AGGTGACGCTGGTGGAGTCTGGGGAGGCGGTGCTCCAGCTGGAGAGTCCCTGAGACTCT 61

QY      62 CCTGTGACGCTCTGGATTCACTTCACTAGTATGAGTGCAGTGGGTCCCGCAGGCTC 121
DB      62 CCTGTGACGCTCTGGATTCACTTCACTAGTATGAGTGCAGTGGGTCCCGCAGGCTC 121

QY      122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGGAATTAATAATACTATG 181
DB      122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGGAATTAATAATACTATG 181
```


TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
FILE REFERENCE: ABGENIX 052A
CURRENT APPLICATION NUMBER: US/10/665,383
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: 60/411,137
PRIOR FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 379
TYPE: DNA
ORGANISM: homo sapiens
US-10-665-383-13

Query Match 84.2%; Score 320.8; DB 17; Length 379;
Best Local Similarity 92.1%; Pred. No. 8.2e-94;
Matches 350; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 2 AGGTGAGCTGCTCCGAGTCTGGGGAGGCGCTGGTCCAGCTGGAGAGTCCCTGAGACTCT 61
DB 2 AGGTGAGCTGCTGGAGTGGGGAGGCGCTGGTCCAGCTGGAGAGTCCCTGAGACTCT 61
QY 62 CCGTGTGACGCTCTGGATTCACTTCAGTAGTATGAGCACTGGGTCGCGCAGGCTC 121
DB 62 CCGTGTGACGCTCTGGATTCACTTCAGTAGTATGAGCACTGGGTCGCGCAGGCTC 121
QY 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAGTAATAATATATG 181
DB 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATGATGAGAGTAATAATATATG 181
QY 182 CAGACTCCGTGAAGGGCGGATTCACTTCAGTAGTATGAGCACTGGGTCGCGCAGGCTC 241
DB 182 CAGACTCCGTGAAGGGCGGATTCACTTCAGTAGTATGAGCACTGGGTCGCGCAGGCTC 241
QY 242 TGCATAATGAACAGCTGAGAGTGAAGCAACGCGCTGTATTAATGCGAAGATATG 301
DB 242 TGCATAATGAACAGCTGAGAGTGAAGCAACGCGCTGTATTAATGCGAAGATATG 301
QY 302 GGTGGGGCAGTGGCTGAGAGCCTTACTACTACGATGAGAGTCTGGGGCCAAAGGA 361
DB 302 GAT---ACAGATATGCTGTTACTACTACGATGAGAGTCTGGGGCCAAAGGA 358
QY 362 CCACGGTCAACCGTCTCTCA 381
DB 359 CCACGGTCAACCGTCTCTCA 378

RESULT 15
US-10-269-711-10

Sequence 10, Application US/10269711
Publication No. US20040071694A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Devries, Peter J.
APPLICANT: Reilly, Edward B.
APPLICANT: Ostrow, Dave
APPLICANT: Weiler, James
TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
FILE REFERENCE: 6989 US 01
CURRENT APPLICATION NUMBER: US/10/269,711
CURRENT FILING DATE: 2002-10-14
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 370
TYPE: DNA
ORGANISM: Homo sapiens
US-10-269-711-10

Query Match 84.1%; Score 320.4; DB 16; Length 370;
Best Local Similarity 92.6%; Pred. No. 1.1e-93;

Matches 352; Conservative 0; Mismatches 16; Indels 12; Gaps 1;
QY 2 AGGTGAGCTGCTCCGAGTCTGGGGAGGCGCTGGTCCAGCTGGAGAGTCCCTGAGACTCT 61
DB 2 AGGTGAGCTGCTGGAGTGGGGAGGCGCTGGTCCAGCTGGAGAGTCCCTGAGACTCT 61
QY 62 CCGTGTGACGCTCTGGATTCACTTCAGTAGTATGAGCACTGGGTCGCGCAGGCTC 121
DB 62 CCGTGTGACGCTCTGGATTCACTTCAGTAGTATGAGCACTGGGTCGCGCAGGCTC 121
QY 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAGTAATAATATATG 181
DB 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAGTAATAATATATG 181
QY 182 CAGACTCCGTGAAGGGCGGATTCACTTCAGTAGTATGAGCACTGGGTCGCGCAGGCTC 241
DB 182 CAGACTCCGTGAAGGGCGGATTCACTTCAGTAGTATGAGCACTGGGTCGCGCAGGCTC 241
QY 242 TGCATAATGAACAGCTGAGAGTGAAGCAACGCGCTGTATTAATGCGAAGATATG 301
DB 242 TGCATAATGAACAGCTGAGAGTGAAGCAACGCGCTGTATTAATGCGAAGATATG 297
QY 302 GGTGGGGCAGTGGCTGAGAGCCTTACTACTACGATGAGAGTCTGGGGCCAAAGGA 361
DB 298 -----CAGGTGAGAGTACGTCTACGACTACGATGAGAGTCTGGGGCCAAAGGA 349
QY 362 CCACGGTCAACCGTCTCTCA 381
DB 350 CCACGGTCAACCGTCTCTCA 369

Search completed: December 7, 2004, 14:26:30
Job time: 328.469 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 06:11:35 ; Search time 2223.46 Seconds
(without alignments)
6244.126 Million cell updates/sec

Title: US-09-403-107-143_COPY_1_381
Perfect score: 381
Sequence: 1 gagggcgacgtcgtcgagtc.....ccacggtcacgcctctcctca 381

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues
Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_hlc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_g881.*
9: gb_g882.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	319.2	83.8	516	2	AM401728 UI-HF-BKO
2	308	80.8	750	2	BF976111 602244955
3	305.4	80.2	802	4	BG756245 602713557
4	302.4	79.4	536	2	AM402624 UI-HF-BKO
5	299.8	78.7	511	2	AM402453 UI-HF-BKO
6	298.4	78.3	958	4	BG757665 602711255
7	297.8	78.2	740	4	BG757947 602711983
8	297.8	78.2	741	4	BG754024 602709552
9	297.6	78.1	1007	4	BM914489 AGENCOURT
10	294	77.2	663	4	BG686759 602650729
11	293	76.9	912	4	BG756211 602713521
12	292.2	76.7	846	4	BG755572 602716255
13	292	76.6	876	4	BG758406 602712604
14	292	76.6	907	5	BQ898892 AGENCOURT
15	291.6	76.5	788	4	BG342203 602462979
16	291.2	76.4	878	4	BG340648 602462226
17	291.2	76.4	870	4	BG759649 602713342
18	291.2	76.4	964	2	BF663281 602144406
19	291.2	76.4	991	2	BF974524 602243430
20	291.2	76.4	1010	2	BF663436 602144593
21	290	76.1	930	4	BG755605 602716292
22	289.4	76.0	899	5	BQ420418 AGENCOURT
23	289.4	76.0	1228	4	BM920476 AGENCOURT
24	287.8	75.5	456	4	BG503730 602549705

25	287.8	75.5	902	5	BX436850
26	287.8	75.5	991	6	CD515249
27	287.2	75.4	413	5	BX344075
28	285.6	75.0	942	5	BQ711102
29	284.4	74.6	894	5	BQ708235
30	283.8	74.5	430	5	BX480277
31	283.6	74.4	979	5	BQ708029
32	282.8	74.2	761	4	BG757080
33	281.4	73.9	621	6	CD687626
34	279.2	73.3	648	6	CD691229
35	278	73.0	907	5	BG685787
36	278	73.0	1001	4	BM914366
37	278	73.0	606	6	CD685360
38	277.2	72.8	503	2	AM402572
39	277	72.7	881	4	BG686259
40	277	72.7	881	4	BG686259
41	276.2	72.5	509	6	CD684864
42	275.8	72.4	923	5	BQ711542
43	275.6	72.3	918	5	BQ710537
44	275.6	72.3	962	5	BQ706534
45	274.8	72.1	413	5	BX399298

ALIGNMENTS

RESULT 1
AM401728 516 bp mRNA linear EST 16-FEB-2000
LOCUS UI-HF-BKO-aaf-f-12-0-UI.r1 NIH MGC_36 Homo sapiens CDNA clone
DEFINITION IMAGE:3053711 5', mRNA sequence.

ACCESSION AM401728
VERSION AM401728.1 GI:6920414
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS 1 (bases 1 to 516)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www-bio.liml.gov/bdrip/image/image.html
Seq primer: M13 Forward.

FEATURES

source
1..516
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3053711"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/lab_lib="NIH MGC 36"
/note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldi, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 83.8%; Score 319.2; DB 2; Length 516;
Best Local Similarity 91.8%; Pred. No. 4,7e-83;

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.lnl.gov/bdir/image/image.html
Seq primer: M13 Forward.

FEATURES

source

1..511
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3054479"
/issue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_1lb="NIH MGC 36"
/note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI; constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 78.7%; Score 299.8; DB 2; Length 511;
Best Local Similarity 88.3%; Pred. No. 2.5e-77;
Matches 338; Conservative 0; Mismatches 42; Indels 3; Gaps 1;

2 AGGTGAGCTGCTGAGCTGTGGGGAGGCTGTGTCAGCTGGAGGCTCCCTGAGACTCT 61
96 AGGTGAGCTGCTGAGCTGTGGGGAGGCTGTGTCAGCTGGAGGCTCCCTGAGACTCT 155
62 CCGTGTGAGCTGCTGAGCTGTGGGGAGGCTGTGTCAGCTGGAGGCTCCCTGAGACTCT 121
156 CCGTGTGAGCTGCTGAGCTGTGGGGAGGCTGTGTCAGCTGGAGGCTCCCTGAGACTCT 215
122 CAGGCAAGGGGCTGAGAGTGGGGAGGCTGTGTCAGCTGGAGGCTCCCTGAGACTCT 181
216 CAGGCAAGGGGCTGAGAGTGGGGAGGCTGTGTCAGCTGGAGGCTCCCTGAGACTCT 275
182 CAGACTCCGTGAGAGGCTGAGAGTGGGGAGGCTGTGTCAGCTGGAGGCTCCCTGAGACTCT 241
276 CAGACTCCGTGAGAGGCTGAGAGTGGGGAGGCTGTGTCAGCTGGAGGCTCCCTGAGACTCT 335
242 TGCAGATGAAAGAGCTGAGAGTGGGGAGGCTGTGTCAGCTGGAGGCTCCCTGAGACTCT 298
336 TGCAGATGAAAGAGCTGAGAGTGGGGAGGCTGTGTCAGCTGGAGGCTCCCTGAGACTCT 395
299 TGGGCTGGGGAGGCTGAGAGTGGGGAGGCTGTGTCAGCTGGAGGCTCCCTGAGACTCT 358
396 GGGGAGCGTGAAGTGAAGTGGGGAGGCTGTGTCAGCTGGAGGCTCCCTGAGACTCT 455
359 GAGACAGGCTGAGAGTGGGGAGGCTGTGTCAGCTGGAGGCTCCCTGAGACTCT 381
456 GAGACAGGCTGAGAGTGGGGAGGCTGTGTCAGCTGGAGGCTCCCTGAGACTCT 478

RESULT 6
BG757665 958 bp mRNA linear EST 15-MAY-2001
LOCUS 602711255F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:485161 5',
DEFINITION mRNA sequence.
ACCESSION BG757665
VERSION BG757665.1 GI:14068318
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbe-remail.nih.gov

FEATURES

source

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://www.bio.lnl.gov>
Plate: LCM1694 row: n column: 14
High quality sequence stop: 799.

ORIGIN

Query Match 78.3%; Score 298.4; DB 4; Length 958;
Best Local Similarity 88.4%; Pred. No. 7.4e-77;
Matches 336; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

2 AGGTGAGCTGCTGAGCTGTGGGGAGGCTGTGTCAGCTGGAGGCTCCCTGAGACTCT 61
122 AGGTGAGCTGCTGAGCTGTGGGGAGGCTGTGTCAGCTGGAGGCTCCCTGAGACTCT 181
62 CCGTGTGAGCTGCTGAGCTGTGGGGAGGCTGTGTCAGCTGGAGGCTCCCTGAGACTCT 121
182 CCGTGTGAGCTGCTGAGCTGTGGGGAGGCTGTGTCAGCTGGAGGCTCCCTGAGACTCT 241
122 CAGGCAAGGGGCTGAGAGTGGGGAGGCTGTGTCAGCTGGAGGCTCCCTGAGACTCT 181
242 CAGGCAAGGGGCTGAGAGTGGGGAGGCTGTGTCAGCTGGAGGCTCCCTGAGACTCT 301
182 CAGACTCCGTGAGAGGCTGAGAGTGGGGAGGCTGTGTCAGCTGGAGGCTCCCTGAGACTCT 241
302 GAGACTCCGTGAGAGGCTGAGAGTGGGGAGGCTGTGTCAGCTGGAGGCTCCCTGAGACTCT 361
242 TGCAGATGAAAGAGCTGAGAGTGGGGAGGCTGTGTCAGCTGGAGGCTCCCTGAGACTCT 301
362 TGCAGATGAAAGAGCTGAGAGTGGGGAGGCTGTGTCAGCTGGAGGCTCCCTGAGACTCT 418
302 GGTGGGGAGGCTGAGAGTGGGGAGGCTGTGTCAGCTGGAGGCTCCCTGAGACTCT 361
419 GGTGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 478
362 CCAAGTACCGCTGCTCTCA 381
479 CCAAGTACCGCTGCTCTCA 498

RESULT 7
BG757947 740 bp mRNA linear EST 15-MAY-2001
LOCUS 602714983F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4854932 5',
DEFINITION mRNA sequence.
ACCESSION BG757947
VERSION BG757947.1 GI:14068600
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
1 (bases 1 to 740)
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LNCM1703 row: f column: 21
High quality sequence stop: 736.
Location/Qualifiers

FEATURES
source
1..740
/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4854932"
/issue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH-MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;
Site: 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC library."

ORIGIN

Query Match 78.2%; Score 297.8; DB 4; Length 740;
Best Local Similarity 86.4%; Pred. No. 1.1e-76;
Matches 329; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

1 GAGGTGACAGCTGCTGAGTCTGGGGAGGCGCTGTCAGCTGGAGGTCCTCGAGATC 60
81 GAGGTGACAGCTGCTGAGTCTGGGGAGGCGCTGTCAGCTGGAGGTCCTCGAGATC 140
61 TCCTGTGACAGCTCTGAGTTCACCTTCAGTAGCTATGAGCAGCTGGGTCGCGCAGGCT 120
141 TCCTGTGACAGCTCTGAGTTCACCTTCAGTAGCTATGAGCAGCTGGGTCGCGCAGGCT 200
121 CCAGGCAAGGGGCTGAGAGTGGTGGCAGTTATCATATGATGAGAACTAATAACTAT 180
201 CCAGGCAAGGGGCTGAGAGTGGTGGTTCATATCATATGAGTAACTAATAACTAT 260
181 GCAGACTCCGTGAAGGGCGGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTAT 240
261 GCAGACTCTGTGAAGGGCGGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTAT 320
241 CTGCAATGAAGAGCTGAGAGCTGAGACAGCGCTGTATTACTGTGGAAAGATATG 300
321 CTGCAATGAAGAGCTGAGAGCTGAGACAGCGCTGTATTACTGTGGAAAGATATG 380
301 GGGTGGGAGAGTGGCTGAGAGCTGAGACCTTACTACTAGAGTATGAGAGCTGGGGCCAAAGG 360
381 ATATATTGTAGTAGTACACAGCTGCTACTACTAGAGTATGAGAGCTGGGGCCAAAGG 440
361 ACCACGTCACCTCTCTCTCA 381
441 ACCACGTCACCTCTCTCTCA 461

RESULT 8
BG754024 741 bp mRNA linear EST 15-MAY-2001
LOCUS BG754024
DEFINITION 602709552F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4846117 5',

ACCESSION
BG754024
VERSION
BG754024.1 GI:14064677
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
1 (bases 1 to 741)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LNCM1686 row: g column: 14
High quality sequence stop: 735.
Location/Qualifiers

FEATURES
source
1..741
/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4846117"
/issue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH-MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;
Site: 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC library."

ORIGIN

Query Match 78.2%; Score 297.8; DB 4; Length 741;
Best Local Similarity 86.4%; Pred. No. 1.1e-76;
Matches 329; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

1 GAGGTGACAGCTGCTGAGTCTGGGGAGGCGCTGTCAGCTGGAGGTCCTCGAGATC 60
81 GAGGTGACAGCTGCTGAGTCTGGGGAGGCGCTGTCAGCTGGAGGTCCTCGAGATC 140
61 TCCTGTGACAGCTCTGAGTTCACCTTCAGTAGCTATGAGCAGCTGGGTCGCGCAGGCT 120
141 TCCTGTGACAGCTCTGAGTTCACCTTCAGTAGCTATGAGCAGCTGGGTCGCGCAGGCT 200
121 CCAGGCAAGGGGCTGAGAGTGGTGGCAGTTATCATATGATGAGAACTAATAACTAT 180
201 CCAGGCAAGGGGCTGAGAGTGGTGGTTCATATCATATGAGTAACTAATAACTAT 260
181 GCAGACTCCGTGAAGGGCGGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTAT 240
261 GCAGACTCTGTGAAGGGCGGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTAT 320
241 CTGCAATGAAGAGCTGAGAGCTGAGACAGCGCTGTATTACTGTGCGAAAGATATG 300
321 CTGCAATGAAGAGCTGAGAGCTGAGACAGCGCTGTATTACTGTGCGAAAGATATG 380
301 GGGTGGGAGAGTGGCTGAGAGCTGAGACCTTACTACTAGAGTATGAGAGCTGGGGCCAAAGG 360
381 ATATATTGTAGTAGTACACAGCTGCTACTACTAGAGTATGAGAGCTGGGGCCAAAGG 440
361 ACCACGTCACCTCTCTCTCA 381

Db		441	ACCAAGGTACCGTCTCCTCA	461	
	RESULT 9				
	BM914489				
	LOCUS				
	DEFINITION	AGENCOURT 6615377 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5480167			
	ACCESSION	BM914489			
	VERSION	BM914489.1 GI:19364868			
	KEYWORDS	EST.			
	SOURCE	Homo sapiens (human)			
	ORGANISM	Homo sapiens			
	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
	TITLE	NIH-MGC http://mgc.ncl.nih.gov/.			
	JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)			
	COMMENT	Unpublished (1999)			
		Contact: Robert Strausberg, Ph.D.			
		Email: cgapbs-rt@mail.nih.gov			
		Tissue Procurement: Dr. Mark Watson			
		cDNA Library Preparation: Rubin Laboratory			
		cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)			
		DNA Sequencing by: Agencourt Bioscience Corporation			
		Clone distribution: MGC clone distribution information can be			
		found through the I.M.A.G.E. Consortium/LNLN at:			
		http://image.llnl.gov			
		Plate: LNCM2002 row: j column: 08			
		High quality sequence stop: 638.			
	FEATURES				
	source	location/Qualifiers			
		1..1007			
		/organism="Homo sapiens"			
		/mol_type="mRNA"			
		/db_xref="caxon:9606"			
		/clone="IMAGE:5480167"			
		//lab_host="VDHI0B (phage-resistant)"			
		/clone_lib="NIH MGC_113"			
		/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:"			
		ECORI; cDNA made by oligo-dT priming. Directionally cloned			
		into ECORI/XhoI sites using the following 5' adaptor:			
		GCGCAGAG(G). Library constructed by Ling Hong in the			
		laboratory of Gerald M. Rubin (University of California,			
		Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and			
		NIH-MGC Library."			
	ORIGIN				
	Query Match	78.1%; Score 297.6; DB 4; Length 1007;			
	Best Local Similarity	86.9%; Pred. No.13e-76;			
	Matches	346; Conservative 0; Mismatches 34; Indels 18; Gaps 1;			
Oy	2	AGGTCACAGCTGCTCCAGTCTGGGGGAGGCCCTGATCCACTTGAGAGCTCT 61			
Db	125	AGGTGACAGCTGCTGGAAGTCTGGGGGAGGCCGTAAGTCAAGCTGGGGGGCTCTGAGACTCT 184			
Oy	62	CCTGTGACAGCTTGGAATTACCTTCAGTAGCTATGCGATGCGATCGGATCGCAGAGCTC 121			
Db	185	CCTGTGACAGCTTGGAATTACCTTCAGTAGCTATGCGATGCGATCGGATCGCAGAGCTC 244			
Oy	122	CAGGAAAGGGGCTGAGAGTGGGGTGGGAGTTATATCATATGAGAAAGTAAATAATATCTATG 181			
Db	245	CAGGAAAGGGGCTGAGAGTGGGGTGGGAGTTATATCGGTATGAGAAAGTAAATAATATCTATG 304			
Oy	182	CAGA-TCTCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCACAGAACCGCTGATC 241			
Db	305	CAGATCTCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCACAGAACCGAGATATC 364			
Oy	242	TGCAAAATGAACAGCTGAGAGCTGAGACACAGCGCTGTGATTTACTGTGCGAAGATATGG 301			
Db	365	TGCAAAATGAACAGCTGAGAGCTGAGACACAGCGCTGTGATTTACTGTGCGAAGATTTCT 424			
Oy	302	GGTGGGGCAGTGGCTGAGAAC--CTACTACTACTACGGTATGG 343			

Db	425		ATTGTTGGTGTGTAGCTGCTTCCTCGTGAGATCCGCATTTCACCTTA	CTTACTACTTCACTACATG	484
Oy	344		ACGTTCTGGGGCCAAAGGACCAACGATCAGCTTCCTCTCA		381
Db	485		ACGTTCTGGGGCAAAGGACCAACGATCACCCTCTCTCA		522
RESULT 10	BG686759				
LOCUS	BG686759				
DEFINITION	602650729P1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763215 5', mRNA sequence.				
ACCESSION	BG686759				
VERSION	BG686759.1				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (baes 1 to 663)				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: LILCM1618 row: 1 column: 08 High quality sequence stop: 659.				
FEATURES	Location/Qualifiers				
SOURCE	1..663				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="IMAGE:4763215"				
	/tissue_type="Primary B-cells from tonsils (cell line)"				
	/lab_host="RDH10B (phage-resistant)"				
	/clone_id="NIH_MGC_48"				
	/note="Organ: B-cells; Vector: pOTB7; Site:1; XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >50bp for average insert size 1.8kb. Library constructed by Lin Hong in the laboratory of Gerald W. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."				
Query Match	77.2%; Score 294;				
Best Local Similarity	87.9%; Pred. No. 1.4e-75;				
Matches 334;	Conservative 0; Mismatches 40; Indels 6; Gaps. 1				
Oy	2		AGGTGACACTGCTGAGTCTGGAGGAGGCCGTGATCCAGCGTCCCGAAGCTCT		61
Db	129		AGGTGACACTGATGAGTCTGGAGGAGGCCGTGATCCAGCGTCCCGAAGCTCT		188
Oy	62		CCTGTGACAGCTCTGAGATTCACTTCAGTAGCTATGATGCACATCGGGTCCGACAGCTC		121
Db	189		CCTGTGACAGCTCTGAGATTCACTTCAGTAGCTATGATGCATCGGGTCCGACAGCTC		248
Oy	122		CAGGCAAGGGGCTGAGAGTGGGTGGCAGTTATATCATATGATGAAGTATAATAATCTATG		181
Db	249		CAGGCAAGGGGCTGAGAGTGGGTGGCAGTTATATCATATGATGAAGCAATAATACTACG		308
Oy	182		CAGACTCCGTGAAGGGCCGATTTCACATCTCCAGAGAACAATTCAGAAACGCTGATC		241

Db 309 CAGACTCCGTAAGGGCCGATTTCACATCTCCAGAGACAATTCAGAAACAGCTGTATC 368
Qy 242 TCGAATGAACAGCTGAGAGTGAAGACACGGCTGTGATTAATCTGTGCAAAAGATATG 301
Db 369 TCGAATGAACAGCTGAGAGTGAAGACACGGCTGTGATTAATCTGTGCAAGATCTTT 428
Qy 302 GGTGGGGGAGTGGCTGAGAGCCCTACTACTACTAGCATAGCATGAGCTGGGGGCAAGGGA 361
Db 429 TTTCGATTAAGCATGTGCTGGCCATCGGAGTACCTCG3-----CTACTGGGGCCAGGGA 482
Qy 362 CCAGGTCAACCTGTCTCTCA 381
Db 483 CCTGTGCAACCTGTCTCTCA 502

RESULT 11
Bg756211 912 bp mRNA linear EST 15-MAY-2001
LOCUS 602713521F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853837 5',
DEFINITION mRNA sequence.
ACCESSION BG756211 GI:14066864
VERSION BG756211.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.jnl.gov
Plate: LNCMI700 row: 1 column: 06
High quality sequence stop: 889.
Location/Qualifiers
1. 912
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4853837"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

ORIGIN
Query Match 76.9%; Score 293; DB 4; Length 912;
Best Local Similarity 95.3%; Pred. No. 2.9e-75;
Matches 302; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 2 AGGTGAGCTGCTCGAGTCTGGGGGAGGCTGTGTCAGCTGGAGAGTCCCTAGACTCT 61
Db 121 AGGTGAGCTGCTCGAGTCTGGGGGAGGCTGTGTCAGCTGGAGAGTCCCTAGACTCT 180
Qy 62 CCTGTGAGGCTCTGATTCACCTTCAAGTATGAGCAATGAGCTGGGTCGGCAGAGCTC 121
Db 181 CCTGTGAGGCTCTGATTCACCTTCAAGTATGAGCAATGAGCTGGGTCGGCAGAGCTC 240

Qy 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGAGTAATAAATCTANG 181
Db 241 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGAGTAATAAATCTANG 300
Qy 182 CAGACTCCGTAAGGGCCGATTACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 241
Db 301 CAGACTCCGTAAGGGCCGATTACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 360
Qy 242 TCGAATGAACAGCTGAGAGTGAAGACACGGCTGTGATTAATCTGTGCAAAAGATATG 301
Db 361 TCGAATGAACAGCTGAGAGTGAAGACACGGCTGTGATTAATCTGTGCAAAAGATATG 420
Qy 302 GGTGGGGGAGTGGCTG 318
Db 421 TGCATTAAGCATGTGCTGG 437

RESULT 12
Bg755572 846 bp mRNA linear EST 15-MAY-2001
LOCUS 602716255F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4856628 5',
DEFINITION mRNA sequence.
ACCESSION BG755572
VERSION BG755572.1 GI:14066225
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.jnl.gov
Plate: LNCMI707 row: m column: 13
High quality sequence stop: 752.
Location/Qualifiers
1. 846
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4856628"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

ORIGIN
Query Match 76.7%; Score 292.2; DB 4; Length 846;
Best Local Similarity 95.8%; Pred. No. 4.9e-75;
Matches 300; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 2 AGGTGAGCTGCTCGAGTCTGGGGGAGGCTGTGTCAGCTGGAGAGTCCCTAGACTCT 61
Db 130 AGGTGAGCTGCTCGAGTCTGGGGGAGGCTGTGTCAGCTGGAGAGTCCCTAGACTCT 189

OY		62	CCTGTGACAGCCCTTGATTCACCTTCAAGACTAATGGCATGCAGCGGCCGACAGGCTC	122
Dd		190	CCTGTGACAGCCCTTGATTCACCTTCAAGACTAATGGCATGCAGCGGCCGACAGGCTC	249
OY		122	CAGGCAAGGGGCGCTGAGTGGTGGCAGTTATATCATATGANTGAATAAATATCTATG	181
Dd		250	CAGGCAAGGGGCGCTGAGTGGTGGCAGTTATATCATATGANTGAATAAATATCTATG	309
OY		182	CAGAATTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAAGAACAGCTGTATC	241
Dd		310	CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAAGAACAGCTGTATC	369
OY		242	TGCAAAATGAACAGCCTGAGAGCTGAGAGACAAGCGCTGTATTACTGTGGCAAAATATG	301
Dd		370	TGCAAAATGAACAGCCTGAGAGCTGAGAGACAAGCGCTGTATTACTGTGGCAAAATATG	429
OY		302	GGTGGGGCAGTTG	314
Dd		430	TCTGAGGGAGTTG	442
RESULT 13				
LOCUS	Bg758406	876 bp	mRNA	linear EST 15-MAY-2001
DEFINITION	602712604F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853016 5', mRNA sequence.			
ACCESSION	Bg758406			
VERSION	Bg758406.1 GI:14069059			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 876) NIH-MGC http://mgi.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)			
AUTHORS	Contact: Robert Strausberg, Ph.D.			
TITLE	Email: cgabbs@mail.nih.gov			
JOURNAL	Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: Ling Hong/Rubin Laboratory DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: LILCM1698 row: 5 column: 01 High quality sequence stop: 856.			
COMMENT	Location/Qualifiers			
	1..876			
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/clone="IMAGE:4853016"			
	/tissue_type="primary B-cells from tonsils (cell line)"			
	/lab_host="DH10B (phage-resistant)"			
	/clone_lib="NIH_MGC_48"			
	/note="Organ: B-cell; Vector: pOTB7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCGCAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald W. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."			
FEATURES				
SOURCE				
ORIGIN				
Query Match	76.6%; Score 292; DB 4; Length 876;			
Best Local Similarity	85.5%; Pred. No. 5.7e-75;			
Matches 325; Conservative	0; Mismatches 55; Indels 0; Gaps 0;			
2 AGGTGACAGCTGCTGAGTCTGGGGAGGCGCTGATCCAGCTGGAGAGTCCCTGAGACTCT 61				

Db	122	AGGTGCATTGTGGAGTCTGGGGGAGGCGGTGTCCACCTCTGGGGGGTCCCTAAGACTCT	181
QY	62	CCTGTGCAGCCTCTGGATTCACTTCAGTAGCTATGGCATGCACTGGGTCCGCGCAGGCTC	121
Db	182	CCTGTGCAGCCTCTGGGGCTCAACCTTCGTACTTGGCATGTGACACTGGGTCCGCGCAGGCTC	241
QY	122	CAGGCAAGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTATAAATCTATG	181
Db	242	CAGGCAAGGGCTGGAGTGGGTGGCCTTAATTCCAGCATGATGGAAAGTAAACGAAGCTATA	301
QY	182	CAGACTCCTGTAAAGGCCGATTCAACCATCTCCAGAGCAATTCGAAGAACACGCTGTATC	241
Db	302	GAGACTCCTGTAAAGGCCGATTCAACCATCTCCAGAGCAATTCGAAGAACACGCTGTATC	361
QY	242	TGCAAAATGAACAGCCTGAGACTGAGACAAGCGCGTGTATTACTGTGCGAAAGATATGG	301
Db	362	TGCAAAATGAACACTGAGAGCTGAGACTGGCGTGTATCACTGTGCGAAAGACCGTA	421
QY	302	GGTGGGGCAGTGGCTGAGACCTTAATACTAATAAGTATGACGCTGTGGGCCCAAGGA	361
Db	422	CGATTTTGGAGTGGTCCGTGACAGTTTGTACTACGATATGACGCTGTGGGCCCAAGGA	481
QY	362	CCACGTCACCGTCTCTCA 381	
Db	482	CCACGTCACCGTCTCTCA 501	

```

RESULT 14
LOCUS      BO898892
DEFINITION BO898892
ACCESSION  BO898892
VERSION     BO898892
KEYWORDS    BO898892.1  GI:22290906
SOURCE      EST.
ORGANISM    Homo sapiens (human)
REFERENCE   Homo sapiens
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE       Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
COMMENT     1 (bases 1 to 907)
            NIH-MGC http://mgs.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgabs-rc@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNLN at:
            http://image.lnl.gov
            Plate: LINC2519 row: c column: 18
            High quality sequence stop: 651.
FEATURES
            location/Qualifiers
            1..907

```

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6302153"
/lab_host="DH10B (phage-resistant)"
/clone_1fb="NH_MGC_113"
/notes="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCGCAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

```

ORIGIN

Query Match 76.6%; Score 292; DB 5; Length 907;
Best Local Similarity 86.8%; Pred. No. 5.7e-75;
Matches 335; Conservative 0; Mismatches 45; Indels 6; Gaps 1;

```

QY 2 AGGTGAGCTGCTCGAGTCTGGGGAGGCGCTGTCAGCCTGGAGAGTCCCTGAGACTCT 61
    |||||
DB 125 AGGTACAACTCTGGAGTCTGGGGAGGCGCTGTCAGCCTGGAGAGTCCCTGAGACTCT 184
    |||||
QY 62 CCTGTGACGCTCTGGATTCACTTCACTAGTATGAGTATGAGTATGAGTATGAGTATG 121
    |||||
DB 185 CCTGTGACGCTCTGGATTCACTTCACTAGTATGAGTATGAGTATGAGTATGAGTATG 244
    |||||
QY 122 CAGGCAAGGGGCTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 181
    |||||
DB 245 CAGGCAAGGGGCTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 304
    |||||
QY 182 CAGACTCCGTGAAGGGCGGATTCACCATCTCCAGAGCAATTCAGAGAACAGCGCTGATC 241
    |||||
DB 305 CAGACTCCGTGAAGGGCGGATTCACCATCTCCAGAGCAATTCAGAGAACAGCGCTGATC 364
    |||||
QY 242 TGCATTAATGAACAGCTGAGAGCTGAGAGACAGGCTGTGTATTACTGTGCGAAGAT--- 297
    |||||
DB 365 TGCATTAATGAACAGCTGAGAGCTGAGAGACAGGCTGTGTATTACTGTGCGAAGATCGGG 424
    |||||
QY 298 --ATGGGTTGGGCACTGCTGAGACCTCACTACTACTACTACTACTACTACTACTACTACT 355
    |||||
DB 425 AATTCGGGTTTGTATTATATGATGATGATGATGATGATGATGATGATGATGATGATG 484
    |||||
QY 356 AAGGACCAACAGCTCAGCTCTCTCTCA 381
    |||||
DB 485 AAGGACCAACAGCTCAGCTCTCTCTCA 510
    |||||
```

RESULT 15
LOCUS BG342203 788 bp mRNA linear EST 27-FEB-2001
DERIVATION 602462979F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:457531 5',
RNA sequence.
ACCESSION BG342203
VERSION BG342203.1 GI:13148641
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 788)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
<http://image.llnl.gov>
Plate: LNCM1287 row: m column: 20
High quality sequence stop: 687.
Location/Qualifiers
1..788
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:457531"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/lab_host="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGG(G). Size-selected >500bp

for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 76.5%; Score 291.6; DB 4; Length 788;
Best Local Similarity 95.5%; Pred. No. 7.3e-75;
Matches 300; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

```

QY 2 AGGTGAGCTGCTCGAGTCTGGGGAGGCGCTGTCAGCCTGGAGAGTCCCTGAGACTCT 61
    |||||
DB 129 AGGTGAGCTGCTGGAGTCTGGGGAGGCGCTGTCAGCCTGGAGAGTCCCTGAGACTCT 188
    |||||
QY 62 CCTGTGACGCTCTGGATTCACTTCACTAGTATGAGTATGAGTATGAGTATGAGTATG 121
    |||||
DB 189 CCTGTGACGCTCTGGATTCACTTCACTAGTATGAGTATGAGTATGAGTATGAGTATG 248
    |||||
QY 122 CAGGCAAGGGGCTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 181
    |||||
DB 249 CAGGCAAGGGGCTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 308
    |||||
QY 182 CAGACTCCGTGAAGGGCGGATTCACCATCTCCAGAGCAATTCAGAGAACAGCGCTGATC 241
    |||||
DB 309 CAGACTCCGTGAAGGGCGGATTCACCATCTCCAGAGCAATTCAGAGAACAGCGCTGATC 368
    |||||
QY 242 TGCATTAATGAACAGCTGAGAGCTGAGAGACAGGCTGTGTATTACTGTGCGAAGATATG 301
    |||||
DB 369 TGCATTAATGAACAGCTGAGAGCTGAGAGACAGGCTGTGTATTACTGTGCGAAGATATG 428
    |||||
QY 302 GGTGGGGCAGTGGC 315
    |||||
DB 429 CTGAGGAGATTGAC 442
    |||||
```

Search completed: December 7, 2004, 11:13:49
Job time : 2227.46 secs

QY 121 CCAGGCAAGGGGCTGAGAGTGGGTGGAGATTATATCATATGATGAGTAATAATACTAT 180
DB 121 CCAGGCAAGGGGCTGAGAGTGGGTGGAGATTATATCATATGATGAGTAATAATACTAT 180
QY 181 GCAGACTCCGTGTAAGGGCCGATTCAACATCTCCAGAGACAAATCCAGAAACGCTGTAT 240
DB 181 GCAGACTCCGTGTAAGGGCCGATTCAACATCTCCAGAGACAAATCCAGAAACGCTGTAT 240
QY 241 CTGCAATGAACAGCTGTAGAGCTGAGACACGGCTGTATTATCTGTGCGAAAAGAA 300
DB 241 CTGCAATGAACAGCTGTAGAGCTGAGACACGGCTGTATTATCTGTGCGAAAAGAA 300
QY 301 GGGTACTGGGGCCAGGGAACCTGTGTCACCGTCTCCAGACACCAAGAGCTCCGGAT 360
DB 301 GGGTACTGGGGCCAGGGAACCTGTGTCACCGTCTCCAGACACCAAGAGCTCCGGAT 360
QY 361 GTGTTCCTCTA 372
DB 361 GTGTTCCTCTA 372

RESULT 2
LOCUS BD075295 372 bp DNA linear PAT 27-AUG-2002
DEFINITION Novel method for the production of anti-human antigen receptors and
uses thereof.
ACCESSION BD075295
VERSION BD075295.1 GI:22620898
KEYWORDS JP 2001519824-A/24.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 372)
AUTHORS Kufer, P. and Raum, T.
TITLE Novel method for the production of anti-human antigen receptors and
uses thereof
JOURNAL Patent: JP 2001519824-A 24 23-OCT-2001;
MICROMET AG

COMMENT OS Homo sapiens (human)
PN JP 2001519824-A/24
PD 23-OCT-2001
PF 14-APR-1998 JP 1998543494
PR 14-APR-1997 EP 97106109.8
PI PETER KUFER, TOBIAS RAUM
PC C07K16/00,C07K16/30,A61K39/395
CC Novel method for the production of anti-human antigen CC
receptors and uses
CC thereof
FH Key
FT CDS
Location/Qualifiers
1..372
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

FEATURES
source
Location/Qualifiers
1..372
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 372; DB 6; Length 372;
Best Local Similarity 100.0%; Pred. No. 6.2e-109;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGGGGCACTGCTGAGTCTGGGGAGTCGTGTAACACCTGGGGGTCCTTGAGACTC 60
DB 1 GAGGGGCACTGCTGAGTCTGGGGAGTCGTGTAACACCTGGGGGTCCTTGAGACTC 60
QY 61 TCTGTGACGCTCTGATTCACCTTGATGATATGATCCATGACATCGGTCGCCAGGCT 120
DB 61 TCTGTGACGCTCTGATTCACCTTGATGATATGATCCATGACATCGGTCGCCAGGCT 120
QY 121 CCAGGCAAGGGGCTGAGAGTGGGTGGAGATTATATCATATGATGAGTAATAATACTAT 180
DB 121 CCAGGCAAGGGGCTGAGAGTGGGTGGAGATTATATCATATGATGAGTAATAATACTAT 180

DB 121 CCAGGCAAGGGGCTGAGAGTGGGTGGAGATTATATCATATGATGAGTAATAATACTAT 180
QY 181 GCAGACTCCGTGTAAGGGCCGATTCAACATCTCCAGAGACAAATCCAGAAACGCTGTAT 240
DB 181 GCAGACTCCGTGTAAGGGCCGATTCAACATCTCCAGAGACAAATCCAGAAACGCTGTAT 240
QY 241 CTGCAATGAACAGCTGTAGAGCTGAGACACGGCTGTATTATCTGTGCGAAAAGAA 300
DB 241 CTGCAATGAACAGCTGTAGAGCTGAGACACGGCTGTATTATCTGTGCGAAAAGAA 300
QY 301 GGGTACTGGGGCCAGGGAACCTGTGTCACCGTCTCCAGACACCAAGAGCTCCGGAT 360
DB 301 GGGTACTGGGGCCAGGGAACCTGTGTCACCGTCTCCAGACACCAAGAGCTCCGGAT 360
QY 361 GTGTTCCTCTA 372
DB 361 GTGTTCCTCTA 372

RESULT 3
LOCUS HSA308463 362 bp mRNA linear PRI 06-FEB-2002
DEFINITION Homo sapiens partial mRNA for immunoglobulin heavy chain variable
region (IGHV3 gene), clone TEG4.
ACCESSION AJ308463
VERSION AJ308463.1 GI:12734095
KEYWORDS IGHV3 gene, immunoglobulin heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Jacobin, M.J., Laroche-Traineau, J., Little, M., Keller, A., Peter, K.,
Weischer, M., Nudten, A. and Clotient-Sanchez, G.
TITLE Human IgG monoclonal anti-alpha(IIB)beta(3)-binding fragments
derived from immunized donors using phage display
JOURNAL J. Immunol. 168 (4), 2035-2045 (2002)
MEDLINE 21681719
PUBMED 11823541

REFERENCE 2 (bases 1 to 362)
AUTHORS Clotient-Sanchez, G.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-2001) Clotient-Sanchez G., UMR5533, Cnrs, Hopital
Cardiologique, Av de Magellan, 33604 Pessac, FRANCE

FEATURES
source
Location/Qualifiers
1..362
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TEG4"
/cell_type="B lymphocyte"
/clone_lib="combinatorial scFv IgG TR-PSX81 library"
/rearranged
/note="alphaIIBbeta3 integrin specific antibody"
1..362
/gene="IGHV3"
<1..>362
/gene="IGHV3"
/codon_start=1
/product="immunoglobulin heavy chain variable region"
/protein_id="CAC28931.1"
/db_xref="GI:12734096"
/translation="EVQLVESGGGVQPGVSPRSLRSCAASGFPSSYAMHWYRQAPGK
LEWVAIVISDSNKKYIADSVKGRFTISDINSKNTLYIQMNSLRADDTAVYICARISYF
DYWGQITLVTSASTKA"
1..362
/gene="IGHV3"
/product="immunoglobulin heavy chain variable region"

gene
CDS

V_region

ORIGIN

Query Match 82.1%; Score 305.4; DB 9; Length 362;
Best Local Similarity 92.5%; Pred. No. 2.2e-87;
Matches 334; Conservative 0; Mismatches 21; Indels 6; Gaps 1;

[illegible]

DEFINITION	LOCUS
339 bp mRNA linear	PRI 30-JUN-2004
Human sapiens partial mRNA for IgD immunoglobulin heavy chain variable region (IGHV3-30 gene), clone T3.3.13.	
ACCESSION	
AF627239	
VERSION	
AF627239.1	GI:49523851
KEYWORDS	
IGHV3-30 gene; immunoglobulin heavy chain; variable region.	
SOURCE	
Human sapiens (human)	
ORGANISM	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	
1	
AUTHORS	
Dono, M.	
TITLE	
Characterization of a novel CD5+ B cell population	
JOURNAL	
Unpublished	
REFERENCE	
2 (bases 1 to 339)	
AUTHORS	
Dono, M.	
TITLE	
Direct Submission	
JOURNAL	
Submitted (10-FEB-2004) Dono M., Oncologia Medica C, Istituto Nazionale Ricerca sul Cancro, L.go R. Benzi 10, Italy, 16132, ITALY	
FEATURES	
SOURCE	
Location/Qualifiers	
1..339	
/organism="Homo sapiens"	
/mol_type="mRNA"	
/db_xref="taxon:9606"	
/chromosome="14"	
/clone="T3.3.13"	
/cell_type="B cell"	
/tissue_type="tonsil"	
/rearranged	
/country="Italy"	
1..339	
/gene="IGHV3-30"	
<1..>339	
/gene="IGHV3-30"	
/codon_start=1	
/product="immunoglobulin heavy chain variable region"	
/protein_id="CAF28442.1"	
/db_xref="GI:49523852"	
/translation="QVQLVDSGGGVDPGRSLRLSCAAGTSSYGMMHWROAPGKGCLEWVAIVSDGSSNRYADSVAGRTISDNSKNLYLQNNSLRADPTAVYYCAKHPPTWGQDTLVTVSS"	
gene	
CDS	

Query Match	81.8%	Score 304.4	DB 9	Length 339
Best Local Similarity	93.8%	Pred. No. 4,7e-87		
Matches 317	Conservative	0	Mismatches 21	Indels 0
			Gaps 0	
Query	2	AGGTGACAGCTGCTGAGACTGCGGGAGATCGTGTACAGCCTGGGGGCTCCCTGAGACTCT	61	
Db	2	AGGTGACAGCTGCTGAGACTGCGGGAGAGCGGTGTCCAGCTGGGAGGTCCCTGAGACTCT	61	
Query	62	CTGTGAGAGCCTCGATTACCTTTATGATTTATGATATGCAATGCACTGGGTCCGACAGCTC	121	
Db	62	CTGTGAGAGCCTCGATTACCTTTACCTTCAAGTATGCAATGCACTGGGTCCGACAGCTC	121	
Query	122	CAGGCAAGGGGCTGAGATGGGATGGCAGTTATATCATATGATGTGAAAGTATTAATATCATATG	181	
Db	122	CAGGCAAGGGGCTGAGATGGGATGGCAGTTATATCATATGATGTGAAAGTATTAATATCATATG	181	
Query	182	CAGACTCCGTGAAGAGGCGCATTCACCACTTCGCCAGACCAATTCACAAGAACACGGTATATC	241	
Db	182	CAGACTCCGTGAAGAGGCGCATTCACCACTTCGCCAGACCAATTCACAAGAACACGGTATATC	241	
Query	242	TGCAATATGAACAGCGTTAGAGCTGAGGACACACGGCTGTGTATTTACTGTGCGAAAAAGGAAAG	301	
Db	242	TGCAATATGAACAGCGTTAGAGCTGAGGACACACGGCTGTGTATTTACTGTGCGAAAAAGGAAAG	301	
Query	302	GCTACTGGGGGCAAGGGAAACCTGGTCAACGGATTCCTCA	339	
Db	302	AGACTTGGGGGCAAGGGAAACCTGGTCAACGGATTCCTCA	339	

```

LOCUS          AF035024          339 bp    mRNA    linear    PRI 24-SEP-1999
DEFINITION     Homo sapiens clone MCE11H myosin-reactive immunoglobulin heavy
                chain variable region mRNA, partial cds.
ACCESSION      AF035024
VERSION        AF035024.1  GI:5921600
KEYWORDS
SOURCE
ORGANISM       Homo sapiens (human)
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 339)
                Wu,X., Liu,B., Van der Merwe,P.L., Kalis,N.N., Bernay,S.M. and
                Young,D.C.
TITLE          Myosin-reactive autoantibodies in rheumatic carditis and normal
                fetus
JOURNAL        Clin. Immunol. Immunopathol. 87 (2), 184-192 (1998)
MEDLINE        98277139
PUBMED         9614934
REFERENCE      2 (bases 1 to 339)
                Young,D.C.
TITLE          Direct Submission
JOURNAL        Submitted (19-NOV-1997) Department of Pathology and Laboratory
                Medicine, University of Texas Health Science Center, 6431 Fannin,
                Houston, TX 77030, USA
FEATURES
Source
1..339
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MCE11H"
<1..>339
/note="autoantibody"
/codon_start=1
/product="myosin-reactive immunoglobulin heavy chain
variable region"
/protein_id="AAD56260.1"
/db_xref="GI:5921601"

```

ORIGIN

/translation="EVQLVESGGGVQPCGSLRLSCAAGCTFPSSYGMHWFOAPGK
LEWVAFIRYDGSNKYYADSVKGRFTISRDNSKNTLYLQNMNLSRADTAVYCAKOLNY
WGQGLIVTSS"

Query Match 80.8%; Score 300.6; DB 9; Length 339;
Best Local Similarity 92.9%; Pred. No. 7.9e-86;
Matches 315; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GAGGTGACCTGCTCCAGTCTGGGGAGTCTGATACAGCTGGGGGCTCCCTGAGACTC 60
DB 1 GAGTCACTGCTGATGAGTCTGGGGAGGCTGCTCAGCTGGGGGCTCCCTGAGACTC 60
QY 61 TCTGTGACAGCTCTGATTCACCTTGTATGATTCATGATTCATGATTCATGATTCAT 120
DB 61 TCTGTGACAGCTCTGATTCACCTTGTATGATTCATGATTCATGATTCATGATTCAT 120
QY 121 CCAGGCAAGGGGCTGAGTGGGTGGGAGTTATCATGATGAGTAAATTAATTAATTAAT 180
DB 121 CCAGGCAAGGGGCTGAGTGGGTGGGAGTTATCATGATGAGTAAATTAATTAATTAAT 180
QY 181 GCAGACTCCGTGAAAGGCCGATTCACCATCTCCAGAGACAATTCAGAGACGCTGTAT 240
DB 181 GCAGACTCCGTGAAAGGCCGATTCACCATCTCCAGAGACAATTCAGAGACGCTGTAT 240
QY 241 CTGCAATGAACAGCTGAGAGCTGAGAGACAGGCTGTATTAATCTGTGCAAAAAAGAA 300
DB 241 CTGCAATGAACAGCTGAGAGCTGAGAGACAGGCTGTATTAATCTGTGCAAAAAAGAA 300
QY 301 GGCTACTGGGGCCAGGGAACCTGTGACACCGTCTCTCTCA 339
DB 301 AACTACTGGGGCCAGGGAACCTGTGACACCGTCTCTCTCA 339

RESULT 6
AF15111 376 bp mRNA linear PRI 04-JUN-2000
LOCUS Homo sapiens clone dms immunoglobulin heavy chain variable region
DEFINITION AF15111
mRNA, partial cds.
ACCESSION AF15111
VERSION AF15111.1 GI:4836305
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 376)
Smithson,S.U., Sriyastava,N., Hutchins,W.A. and Westerink,M.A.
Molecular analysis of the heavy chain of antibodies that recognize
the capsular polysaccharide of Neisseria meningitidis in hu-PBMC
reconstituted SCID mice and in the immunized human donor
Mol. Immunol. 36 (2), 113-124 (1999)

REFERENCE
AUTHORS 2 (bases 1 to 376)
Smithson,S.U., Sriyastava,N., Hutchins,W.A. and Westerink,M.A.J.
Direct Submission
Submitted (17-DEC-1998) Medicine, Medical College of Ohio, 3000
Arlington Ave, Toledo, OH 43614, USA
Location/Qualifiers
1. 376
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="dms"
/cell_type="B cell"
/codon_start=1
/product="immunoglobulin heavy chain variable region"
/protein_id="A030387.1"
/db_xref="GI:4836306"

FEATURES
source
1. 376
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="dms"
/cell_type="B cell"
/codon_start=1
/product="immunoglobulin heavy chain variable region"
/protein_id="A030387.1"
/db_xref="GI:4836306"

CDS

/translation="EVQLVESGGGVQPCGSLRLSCAAGCTFPSSYGMHWFOAPGK
LEWVAFIRYDGSNKYYADSVKGRFTISRDNSKNTLYLQNMNLSRADTAVYCAKOLNY
WGQGLIVTSS"

ORIGIN

V_region RGGYWGQGLIVTSSASTKAPSV"
1..294
/note="VJ-23"
J_segment 313..376
/note="JH4b"

Query Match 79.6%; Score 296.2; DB 9; Length 376;
Best Local Similarity 90.5%; Pred. No. 2.1e-84;
Matches 332; Conservative 0; Mismatches 23; Indels 12; Gaps 1;

QY 2 AGGTGACCTGCTCCAGTCTGGGGAGTCTGATACAGCTGGGGGCTCCCTGAGACTCT 61
DB 2 AGGTGACCTGCTCCAGTCTGGGGAGTCTGATACAGCTGGGGGCTCCCTGAGACTCT 61
QY 62 CCTGTGACAGCTCTGATTCACCTTGTATGATTCATGATTCATGATTCATGATTCAT 121
DB 62 CCTGTGACAGCTCTGATTCACCTTGTATGATTCATGATTCATGATTCATGATTCAT 121
QY 122 CAGGCAAGGGGCTGAGTGGGTGGGAGTTATCATGATGAGTAAATTAATTAATTAAT 181
DB 122 CAGGCAAGGGGCTGAGTGGGTGGGAGTTATCATGATGAGTAAATTAATTAATTAAT 181
QY 182 GCAGACTCCGTGAAAGGCCGATTCACCATCTCCAGAGACAATTCAGAGACGCTGTATC 241
DB 182 GCAGACTCCGTGAAAGGCCGATTCACCATCTCCAGAGACAATTCAGAGACGCTGTATC 241
QY 242 TGCATATGAACAGCTGAGAGCTGAGAGACAGGCTGTATTAATCTGTGCAAAAAAGAA 301
DB 242 TGCATATGAACAGCTGAGAGCTGAGAGACAGGCTGTATTAATCTGTGCAAAAAAGAA 301
QY 292 --AAAAGAGAGAGCTGAGAGCTGAGAGACAGGCTGTATTAATCTGTGCAAAAAAGAA 349
DB 302 ATGACAGGGAGGCTGAGAGCTGAGAGACAGGCTGTATTAATCTGTGCAAAAAAGAA 361
QY 350 AGGCTCC 356
DB 362 AGGCCCC 368

RESULT 7
AB063888 345 bp mRNA linear PRI 02-JUL-2002
LOCUS Homo sapiens IGH mRNA for immunoglobulin heavy chain VHDJ region,
partial cds, clone:H238.
DEFINITION AB063888
partial cds, clone:H238.
ACCESSION AB063888.1 GI:21669977
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 345)
Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
Miura,K. and Kurosawa,Y.
Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics
Unpublished
2 (bases 1 to 345)
Kurosawa,Y.
Direct Submission
Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutubake-cho, Toyosake 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/.

REFERENCE
AUTHORS 2 (bases 1 to 345)
Kurosawa,Y.
Direct Submission
Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutubake-cho, Toyosake 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/.

FEATURES
source
1. 345
/organism="Homo sapiens"
/mol_type="mRNA"

/translation="EVQLVESGGGVQPCGSLRLSCAAGCTFPSSYGMHWFOAPGK
LEWVAFIRYDGSNKYYADSVKGRFTISRDNSKNTLYLQNMNLSRADTAVYCAKOLNY
WGQGLIVTSS"

/db xref="taxon:9606"
/clone="H238"
/note="AIMS4"
/note="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
1.345
/gene="IGH"
<1..>345
/gene="IGH"
/codon_start=1
/product="immunoglobulin heavy chain VHDJ region"
/protein_id="BAC01516.1"
/db xref="GI:21669978"
/translation="EVQLVESGGGVQPGKSLRLCAASGFTSSYGMHWROAPKGL
LFWAVISYDSNRYADSVKGRFTISRDNSKNTLYLQNSLRADDAVYYCAKRTG
DYGQGLTVSS"

ORIGIN

Query Match 78.4%; Score 291.8; DB 9; Length 345;
Best Local Similarity 93.3%; Pred. No. 5.6e-83;
Matches 318; Conservative 0; Mismatches 17; Indels 6; Gaps 1;

QY 1 GAGGTGCAGCTGCTCGAGTCTGGGGAGTCTGGTACAGCTGGGGGTCCTGAGACTC 60
DB 1 GAGGTGCAGCTGCTGAGTCTGGGGAGTCTGGTACAGCTGGGGGTCCTGAGACTC 60
QY 61 TCTGTGACGCTCTGGATTACCTTTGATGATTATGATGATGATGATGATGATGAT 120
DB 61 TCTGTGACGCTCTGGATTACCTTTGATGATGATGATGATGATGATGATGATGAT 120
QY 121 CCAGGCAAGGGGCTGAGTGGGTGGGAGTATATATATATATATATATATATATATAT 180
DB 121 CCAGGCAAGGGGCTGAGTGGGTGGGAGTATATATATATATATATATATATATATAT 180
QY 181 GGAAGTCCGTGAGAGGCGGATTCACCATCTCCAGAGCAATTCAGAGAGCGTGTAT 240
DB 181 GGAAGTCCGTGAGAGGCGGATTCACCATCTCCAGAGCAATTCAGAGAGCGTGTAT 240
QY 241 CTGCAATGAAACAGCTGAGAGTGGAGACAGCGCTGTATTTACTGTGCGAAA----- 294
DB 241 CTGCAATGAAACAGCTGAGAGTGGAGACAGCGCTGTATTTACTGTGCGAAA----- 294
QY 295 AAGGAAGGCTACTGGGGCCAGGGAACCTGTGACCGCTGC 335
DB 301 ACTGGGACTACTGGGGCCAGGGAACCTGTGACCGCTGC 341

RESULT 8
LOCUS HSIHVCA 342 bp DNA linear PRI 05-AUG-1999
DEFINITION H.sapiens (VHL) gene for immunoglobulin heavy chain variable
region.
ACCESSION Z31686
VERSION Z31686.1 GI:509782
KEYWORDS immunoglobulin heavy chain; immunoglobulin heavy chain variable
region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Figini,M., Marks,J.D., Winter,G. and Griffiths,A.D.
AUTHORS In vitro assembly of repertoires of antibody chains on the surface
TITLE of phage by renaturation
J. Mol. Biol. 239 (1), 68-78 (1994)
MEDLINE 94254092
PUBMED 8196048
REFERENCE Griffiths,A.D.
AUTHORS Direct Submision
TITLE Submitted (30-MAR-1994) A.D. Griffiths, MRC Centre for Protein
JOURNAL Engineering, Hills Road, Cambridge, CB2 2QH, U.K
FEATURES Location/Qualifiers

source 1.342
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db xref="taxon:9606"
/cell_type="peripheral lymphocyte"
/tissue_type="blood"
/dev stage="adult"
1.342
/note="Protein sequence is in conflict with the conceptual
translation"
/codon_start=1
/product="immunoglobulin heavy chain variable region
(VH-IL) "
/protein_id="CAA83491.1"
/db xref="GI:135143"
/translation="EVQLVESGGGVQPGKSLRLCAASGFTSSYGMHWROAPKGL
LFWAVISYDSNRYADSVKGRFTISRDNSKNTLYLQNSLRADDAVYYCAKRWMD
YMGQGLTVSS"

ORIGIN

Query Match 78.4%; Score 291.6; DB 9; Length 342;
Best Local Similarity 93.5%; Pred. No. 6.5e-83;
Matches 316; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

QY 1 GAGGTGCAGCTGCTCGAGTCTGGGGAGTCTGGTACAGCTGGGGGTCCTGAGACTC 60
DB 1 GAGGTGCAGCTGCTGAGTCTGGGGAGTCTGGTACAGCTGGGGGTCCTGAGACTC 60
QY 61 TCTGTGACGCTCTGGATTACCTTTGATGATTATGATGATGATGATGATGATGAT 120
DB 61 TCTGTGACGCTCTGGATTACCTTTGATGATGATGATGATGATGATGATGATGAT 120
QY 121 CCAGGCAAGGGGCTGAGTGGGTGGGAGTATATATATATATATATATATATATATAT 180
DB 121 CCAGGCAAGGGGCTGAGTGGGTGGGAGTATATATATATATATATATATATATATAT 180
QY 181 GGAAGTCCGTGAGAGGCGGATTCACCATCTCCAGAGCAATTCAGAGAGCGTGTAT 240
DB 181 GGAAGTCCGTGAGAGGCGGATTCACCATCTCCAGAGCAATTCAGAGAGCGTGTAT 240
QY 241 CTGCAATGAAACAGCTGAGAGTGGAGACAGCGCTGTATTTACTGTGCGAAA-----G 297
DB 241 CTGCAATGAAACAGCTGAGAGTGGAGACAGCGCTGTATTTACTGTGCGAAA-----G 297
QY 298 GAAAGTACTGGGGCCAGGGAACCTGTGACCGCTGC 335
DB 301 GGAAGTACTGGGGCCAGGGAACCTGTGACCGCTGC 338

RESULT 9
LOCUS HSE5435 437 bp mRNA linear PRI 15-MAR-1993
DEFINITION H.sapiens rearranged Ig heavy chain variable region (VDJ).
ACCESSION Z14203 X65741
VERSION Z14203.1 GI:30965
KEYWORDS Ig D-segment; Ig heavy chain; Ig J-segment; Ig V-segment; Ig
variable region; immunoglobulin.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Cuisinier,A.M., Gauthier,L., Boubli,L., Fougereau,M. and
AUTHORS Tonnelie,C.
TITLE Mechanisms that generate human immunoglobulin diversity operate
JOURNAL Eur. J. Immunol. 23 (1), 110-118 (1993)
MEDLINE 93122076
PUBMED 8419161
REFERENCE Tonnelie,C.
AUTHORS Direct Submision
TITLE Submitted (09-JUN-1992) C. Tonnelie, Centre d'Immunologie
JOURNAL

CDS

```
<1..>425
/contig="IG1"
/codon_start=3
/product="immunoglobulin heavy chain"
/protein_id="AAS5871.1"
/db_xref="GI:46253798"
/translation="WYFVALLRGVOCQVQVYVSGGGVYVPGGSLRLSCAAGSPTSS
YGMHWYRQPKGLEWAFRTYDGSNRTYADSVKRFITSDNSKNITLYQMSLRAE
DTAVYCAVGFQFNFWGGTLTVSSASPTKPVPLSL"
```

ORIGIN

Query Match 78.0%; Score 290; DB 9; Length 425;
Best Local Similarity 87.2%; Pred. No. 2.2e-82;

Matches 330; Conservative 0; Mismatches 40; Indels 6; Gaps 1;

```
QY 2 AGGTGAGCTGCTGAGTCTGGGGAGTCTGTGTACAGCTGGGGGCTCCGTGAGCTCT 61
    |||||
DB 43 AGGTGAGCTGCTGAGTCTGGGGAGTCTGTGTACAGCTGGGGGCTCCGTGAGCTCT 102
    |||||
QY 62 CCTGTGACGCTCTGTGATTCACTTTGATGATTATGTCATGCACTGGGCTCCGCAAGCTC 121
    |||||
DB 103 CCTGTGACGCTCTGTGATTCACTTTGATGATTATGTCATGCACTGGGCTCCGCAAGCTC 162
    |||||
QY 122 CAGGCAAGGGGCTGAGTGGGGTGGCAGTTATATCATATGATGAGTAATAATAACTATG 181
    |||||
DB 163 CAGGCAAGGGGCTGAGTGGGGTGGCAGTTATATCATATGATGAGTAATAATAACTATG 222
    |||||
QY 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 241
    |||||
DB 223 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 282
    |||||
QY 242 TGCATATGAACAGCTGAGAGCTGAGAGCAACGGCTGTATTTCTGTGCAAA-----A 295
    |||||
DB 283 TGCATATGAACAGCTGAGAGCTGAGAGCAACGGCTGTATTTCTGTGCAAA-----A 342
    |||||
QY 296 AGGAAGCTACTCTGGGGCCAGGGAACCTGTGTACCGCTCTCCAGACACCACCAAGGCTC 355
    |||||
DB 343 TTGGGAATCTTTCTGGGGCCAGGGAACCTGTGTACCGCTCTCCAGACACCACCAAGGCTC 402
    |||||
QY 356 CGGATGTGTCTCTCT 371
    |||||
DB 403 CCAAGTCTTCCCGCT 418
    |||||
```

RESULT 12
AR454086 675 bp DNA linear PAT 20-FEB-2004
LOCUS Sequence 59 from patent US 6680209.
DEFINITION AR454086
ACCESSION AR454086
VERSION AR454086.1 GI:42686933
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 675)
AUTHORS Buechler,J., Valkirs,G., Gray,J. and Lomberg,N.
TITLE Human antibodies as diagnostic reagents
JOURNAL Patent: US 6680209-A 59 20-JAN-2004;
FEATURES
Location/Qualifiers
1..675
source
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 77.6%; Score 288.8; DB 6; Length 675;
Best Local Similarity 87.2%; Pred. No. 5.9e-82;

Matches 333; Conservative 0; Mismatches 37; Indels 12; Gaps 1;

```
QY 2 AGGTGAGCTGCTGAGTCTGGGGAGTCTGTGTACAGCTGGGGGCTCCGTGAGCTCT 61
    |||||
DB 2 AGGTGAGCTGCTGAGTCTGGGGAGTCTGTGTACAGCTGGGGGCTCCGTGAGCTCT 61
    |||||
QY 62 CCTGTGACGCTCTGTGATTCACTTTGATGATTATGTCATGCACTGGGCTCCGCAAGCTC 121
    |||||
```

```
DB 62 CCTGTGACGCTCTGTGATTCACTTTGATGATTATGTCATGCACTGGGCTCCGCAAGCTC 121
    |||||
```

```
QY 122 CAGGCAAGGGGCTGAGTGGGGTGGCAGTTATATCATATGATGAGTAATAATAACTATG 181
    |||||
DB 122 CAGGCAAGGGGCTGAGTGGGGTGGCAGTTATATCATATGATGAGTAATAATAACTATG 181
    |||||
```

```
QY 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 241
    |||||
DB 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 241
    |||||
```

```
QY 242 TGCATATGAACAGCTGAGAGTGGAGACACGGCTGTGTATTAAGTGTGGAATAAAG--- 298
    |||||
DB 242 TGCATATGAACAGCTGAGAGTGGAGACACGGCTGTGTATTAAGTGTGGAATAAAG--- 301
    |||||
```

```
QY 299 -----AAGCTTACTGGGGCCAGGGAACCTGTGTACCGCTCTCCAGACACCACCA 349
    |||||
DB 302 TGGGTAATCTTTGATTTGGGGCCAGGGAACCTGTGTACCGCTCTCCAGACACCACCA 361
    |||||
```

```
QY 350 AGGCTCCGATGTCTCTCT 371
    |||||
DB 362 AGGCTCCGATGTCTCTCT 383
    |||||
```

RESULT 13
AR454102 675 bp DNA linear PAT 20-FEB-2004
LOCUS Sequence 91 from patent US 6680209.
DEFINITION AR454102
ACCESSION AR454102
VERSION AR454102.1 GI:42686949
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 675)
AUTHORS Buechler,J., Valkirs,G., Gray,J. and Lomberg,N.
TITLE Human antibodies as diagnostic reagents
JOURNAL Patent: US 6680209-A 91 20-JAN-2004;
FEATURES
Location/Qualifiers
1..675
source
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 77.6%; Score 288.8; DB 6; Length 675;
Best Local Similarity 87.2%; Pred. No. 5.9e-82;

Matches 333; Conservative 0; Mismatches 37; Indels 12; Gaps 1;

```
QY 2 AGGTGAGCTGCTGAGTCTGGGGAGTCTGTGTACAGCTGGGGGCTCCGTGAGCTCT 61
    |||||
DB 2 AGGTGAGCTGCTGAGTCTGGGGAGTCTGTGTACAGCTGGGGGCTCCGTGAGCTCT 61
    |||||
QY 62 CCTGTGACGCTCTGTGATTCACTTTGATGATTATGTCATGCACTGGGCTCCGCAAGCTC 121
    |||||
DB 62 CCTGTGACGCTCTGTGATTCACTTTGATGATTATGTCATGCACTGGGCTCCGCAAGCTC 121
    |||||
QY 122 CAGGCAAGGGGCTGAGTGGGGTGGCAGTTATATCATATGATGAGTAATAATAACTATG 181
    |||||
DB 122 CAGGCAAGGGGCTGAGTGGGGTGGCAGTTATATCATATGATGAGTAATAATAACTATG 181
    |||||
QY 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 241
    |||||
DB 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 241
    |||||
QY 242 TGCATATGAACAGCTGAGAGTGGAGACACGGCTGTGTATTAAGTGTGGAATAAAG--- 298
    |||||
DB 242 TGCATATGAACAGCTGAGAGTGGAGACACGGCTGTGTATTAAGTGTGGAATAAAG--- 301
    |||||
QY 299 -----AAGCTTACTGGGGCCAGGGAACCTGTGTACCGCTCTCCAGACACCACCA 349
    |||||
DB 302 TGGGTAATCTTTGATTTGGGGCCAGGGAACCTGTGTACCGCTCTCCAGACACCACCA 361
    |||||
QY 350 AGGCTCCGATGTCTCTCT 371
    |||||
```

```

Db      362 AGGGCCCATCGGCTTCCCT 383
RESULT 14
AR454084
LOCUS    AR454084 677 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 55 from patent US 6680209.
ACCESSION AR454084
VERSION  AR454084.1 GI:42686931
KEYWORDS
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 677)
AUTHORS   Buechler,J., Valkirs,G., Gray,J. and Lomborg,N.
TITLE     Human antibodies as diagnostic reagents
JOURNAL   Patent: US 6680209-A 55 20-JAN-2004;
FEATURES
     source
         1..677
         /organism="unknown"
         /mol_type="genomic DNA"

ORIGIN
Query Match      77.5%; Score 288.2; DB 6; Length 677;
Best Local Similarity 86.9%; Pred. No. 9.2e-82;
Matches 333; Conservative 0; Mismatches 38; Indels 12; Gaps 1;

QY      1 GAGGTGACAGTCTGAGTCTGGGGAGTCGTGTAACAGCTGGGGGTCCCTGAGACTC 60
      3 GATGTGACAGTCTGAGTCTGGGGAGTCGTGTAACAGCTGGGGGTCCCTGAGACTC 62
      61 TCTGTGACAGCTCTGAGTCTGGGGAGTCGTGTAACAGCTGGGGGTCCCTGAGACTC 120
      63 TCTGTGACAGCTCTGAGTCTGGGGAGTCGTGTAACAGCTGGGGGTCCCTGAGACTC 122
      121 CCGAGGAAGGGGCTGAGTCTGGGGAGTCGTGTAACAGCTGGGGGTCCCTGAGACTC 180
      123 CCGAGGAAGGGGCTGAGTCTGGGGAGTCGTGTAACAGCTGGGGGTCCCTGAGACTC 182
      181 GCAGACTCGGTGAGGGGCGGATTCACATCTCCAGAGACAATTCAGAGACGCTGTAT 240
      183 GCAGACTCGGTGAGGGGCGGATTCACATCTCCAGAGACAATTCAGAGACGCTGTAT 242
      QY  241 CTGCAATGAGACGCTGAGAGTGAAGACACGGCTGTATTAATCTGTGCGAAAAAG-- 298
      243 CTGCAATGAGACGCTGAGAGTGAAGACACGGCTGTATTAATCTGTGCGAAAAAG-- 302
      QY  299 -----AAGGCTACGGGGGCGAGGGAACCTGTCACGCTCCCTCAGACCCACC 348
      DB  303 ATCGGCTACTTTGACTATTGGGGCGAGGAACTGTGTCACGCTCTCAGCTCCACC 362
      QY  349 AAGGCTCCGAGTGTTCCTCT 371
      DB  363 AAGGGCCCATCGGCTTCCCT 385

RESULT 15
BD185287 1392 bp DNA linear PAT 17-JUN-2003
LOCUS    BD185287
DEFINITION Uses of anti-CTLA-4 antibodies.
ACCESSION BD185287
VERSION  BD185287.1 GI:31877487
KEYWORDS JP 2002371013-A/7.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1392)
AUTHORS   Douglas,C.H. and Mueller,E.E.
TITLE     Uses of anti-CTLA-4 antibodies
JOURNAL   Patent: JP 2002371013-A 7 26-DEC-2002;
PFIZER PRODUCTS INC

```

```

COMMENT OS Homo sapiens (human)
PN      JP 2002371013-A/7
PD      26-DEC-2002
PF      17-MAY-2002 JP 2002142978
PR      23-MAY-2001 US 60/293042
PI      CHARLES HANSSON DOUGLAS, EILEEN ELIOTT MUELLER PC
CC      A61K39/395,A61K38/00,A61P35/00//C07K16/18
CQ      Uses of anti-CTLA-4 antibodies
FT      Key
FT      source
FT      Location/Qualifiers
     source
         1..1392
         /organism="Homo sapiens"
         /mol_type="genomic DNA"
         /db_xref="taxon:9606"

ORIGIN
Query Match      77.3%; Score 287.4; DB 6; Length 1392;
Best Local Similarity 86.8%; Pred. No. 1.9e-81;
Matches 334; Conservative 0; Mismatches 36; Indels 15; Gaps 1;

QY      2 AGGTGACAGTCTGAGTCTGGGGAGTCGTGTAACAGCTGGGGGTCCCTGAGACTCT 61
      59 AGGTGACAGTCTGAGTCTGGGGAGTCGTGTAACAGCTGGGGGTCCCTGAGACTCT 118
      62 CCTGTGACAGCTCTGAGTCTGGGGAGTCGTGTAACAGCTGGGGGTCCCTGAGACTC 121
      119 CTTGTACAGCGCTGAGTCTGGGGAGTCGTGTAACAGCTGGGGGTCCCTGAGACTC 178
      122 CAGGGAAGGGGCTGAGTCTGGGGAGTCGTGTAACAGCTGGGGGTCCCTGAGACTC 181
      179 CAGGGAAGGGGCTGAGTCTGGGGAGTCGTGTAACAGCTGGGGGTCCCTGAGACTC 238
      QY  182 CAGACTCGGTGAGGGGCGGATTCACATCTCCAGAGACAATTCAGAGACGCTGTATC 241
      239 CAGACTCGGTGAGGGGCGGATTCACATCTCCAGAGACAATTCAGAGACGCTGTATC 298
      DB  242 TGCAATGAGACGCTGAGAGTGAAGACACGGCTGTATTAATCTGTGCGAAAAAG-- 300
      299 TGCAATGAGACGCTGAGAGTGAAGACACGGCTGTATTAATCTGTGCGAAAAAG-- 358
      QY  301 -----GGTACTGGGGGCGAGGGAACCTGTCACGCTCCCTCAGACCCACC 346
      DB  359 TCTGGGTTACTTTGACTATTGGGGCGAGGAACTGTGTCACGCTCTCAGCTCCACC 418
      QY  347 CCAAGGCTCCGAGTGTTCCTCT 371
      DB  419 CCAAGGGCCCATCGGCTTCCCT 443

Search completed: December 7, 2004, 08:53:04
Job time : 2105.27 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 22:52:33 ; Search time 314.933 Seconds
(without alignments)
6200.629 Million cell updates/sec

Title: US-09-403-107-145

Perfect score: 372
Sequence: 1 gaggtgacactctgcagc.....ctccgagatgtgtccctcra 372

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 413486 segs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	372	100.0	372	2	AAV68538
2	302.2	81.2	729	12	ADN07003
3	294.8	79.2	396	10	ADC61027
4	290.4	78.1	675	4	AAH41661
5	288.8	77.6	675	4	AAH30007
6	288.8	77.6	675	4	AAH41673
7	288.8	77.6	675	4	AAH41657
8	288.8	77.6	675	4	AAH30003
9	288.8	77.6	675	4	AAH30019
10	288.2	77.5	677	4	AAH41655
11	288.2	77.5	677	4	AAH30001
12	287.8	77.4	1398	10	ADZ28458
13	287.4	77.3	1392	3	AAA46870
14	287.4	77.3	1392	3	AAA46896
15	287.4	77.3	1392	10	AAZ54347
16	287.2	77.2	675	4	AAH41678
17	287.2	77.2	675	4	AAH30024
18	286.4	77.0	660	4	AAH68537
19	286.4	77.0	660	4	AAH31367
20	286.4	76.9	1395	3	AAA46866
21	286				AAH46866 DNA encod

22	286	76.9	1395	3	AAA46894	AAH46894 DNA encod
23	286	76.9	1395	10	AAZ54345	AAZ54345 Human 4.8
24	285.8	76.8	1392	3	AAA46864	AAH46864 DNA encod
25	285.8	76.8	1392	3	AAA46890	AAH46890 CDNA enco
26	285.8	76.8	1392	3	AAA46892	AAH46892 DNA encod
27	285.8	76.8	1392	10	AAZ54341	AAZ54341 Human 4.1
28	285.8	76.8	1392	10	AAZ54343	AAZ54343 Human 4.1
29	285.6	76.8	675	4	AAH30059	AAH30059 TR0005 he
30	285.6	76.8	675	4	AAH30062	AAH30062 TR0005 he
31	284.4	76.5	357	12	AD126655	AD126655 Human ant
32	284.2	76.4	1999	3	AAA46891	AAH46891 DNA encod
33	284.2	76.4	1399	10	AAZ54342	AAZ54342 Human 4.1
34	284	76.3	351	12	AD122042	AD122042 Anti-plat
35	284	76.3	351	12	AD122043	AD122043 Anti-plat
36	284	76.3	675	4	AAH41681	AAH41681 Human int
37	284	76.3	675	4	AAH30027	AAH30027 Anti-IL8
38	283.8	76.3	405	10	ADC61031	ADC61031 Human ant
39	282.4	75.9	351	12	AD122044	AD122044 Anti-plat
40	282.4	75.9	351	12	AD122041	AD122041 Anti-plat
41	282.4	75.9	675	4	AAH41682	AAH41682 Human int
42	282.4	75.9	675	4	AAH41677	AAH41677 Human int
43	282.4	75.9	675	4	AAH41680	AAH41680 Human int
44	282.4	75.9	675	4	AAH30026	AAH30026 Anti-IL8
45	282.4	75.9	675	4	AAH30023	AAH30023 Anti-IL8

ALIGNMENTS

RESULT 1	AAV68538	AAV68538 standard; DNA; 372 BP.
ID	AAV68538	
AC	AAV68538	
AC	AAV68538	
DT	16-FEB-1999	(First entry)
DE	Nucleotide sequence of human D7.2 heavy chain variable region.	
XX	Human; D7.2 heavy chain variable region; receptor; antigen; tumour;	
KW	auto-immune disease; graft rejection; allergy; inflammatory disease;	
KW	endocrine disease; degenerative disease; ss.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	Key	
FT	CDS	
FT	1..372	
FT	/tag= a	
FT	/product= "human D7.2 heavy chain variable region"	
XX	WO9846645-A2.	
XX	22-OCT-1998.	
PD	14-APR-1998; 98WO-EP002180.	
XX	14-APR-1997; 97EP-00106109.	
PR	(KUPE/) KUPE P.	
PA	(RAUM/) RAUM T.	
XX	Kufner P, Raum T;	
PI	WPI; 1998-594564/50.	
DR	P-PDB; AAW80816.	
XX	Production of anti-human antigen receptors - by selecting a combination	
PT	of functionally rearranged VH and VL immunoglobulin chains expressed from	
PT	a recombinant vector.	
XX	Claim 9; Fig 8; 84pp; English.	
PS	This is the nucleotide sequence of the human D7.2 heavy chain variable	
XX		
CC		

XX	DR	WP1; 2003-558954/52.
XX	DR	P-FSDB; ADC61028.
XX	PT	New anti-CD45RB monoclonal antibody, useful for treating an autoimmune disease e.g. multiple sclerosis.
XX	PS	Disclosure; SEQ ID NO 54; 121bp; English.
XX	CC	The invention relates to a novel isolated monoclonal antibody comprising a heavy chain having a sequence chosen from one of 22 fully defined sequences comprising 135-147 amino acids, given in the specification, and is specific for CD45RB antigen. The invention further relates to:
XX	CC	inhibiting cell proliferation associated with the expression of CD45RB antigen; and treating a disease associated with the expression of a CD45RB antigen in a patient. The monoclonal antibody has the activities of immunosuppressive and neuroprotective. The monoclonal antibody is useful for treating the rejection of a mammalian cell, tissue or organ,
XX	CC	especially an autoimmune disease in a mammal, especially a human e.g. multiple sclerosis. This polynucleotide sequence represents a DNA encoding a human protein of the anti-CD45RB monoclonal antibody of the invention.
XX	SO	Sequence 396 BP; 84 A; 92 C; 124 G; 96 T; 0 U; 0 Other;
XX	Query Match	79.2%; Score 234.8; DB 10; Length 396;
XX	Best Local Similarity	92.0%; Pred. No. 3.1e-77;
XX	Matches 311; Conservative	0; Mismatches 27; Indels 0; Gaps 0;
OY	2	AGGTGACACTGTCTGCAGTCTGGGGAGTCGTGTTACAGCGTGGGGGTCCCGAGAATTCT 61
Db	59	AGGTGACACTGTGTGAAGTCTGGGGAGCGGTGTCCAGCTGGAGTCCCTGAGACTCT 118
OY	62	CCTGTGACGCCCTTGATTCACCTTTGATGATTAATGCCATGCACTGGGTCCGCAAGCTC 121
Db	119	CCTGTGACGCCGTGTGATTCACCTTCAGAACTAATGGAATGCACTGGGTCCGCAAGCTC 178
OY	122	CAGGCAAGGGGCTGGAGTGGGTGGCATTTATTCATATGATGGAAGTAAATAATCTATG 181
Db	179	CAGGCAAGGGGCTGGAGTGGGTGGCTTTATTTGATGATGATGGAAGTAAAGATTTCTATG 238
OY	182	CAGACTCCGTGAAGGGGCGGATTCACCATCTCCAGAGACAATTCCAAAGAACAGCGTATC 241
Db	239	CAGGCTCCGTGAAGGGGCGGATTCACCATCTCCAGAGACAATTCCAAAGAACAGCGTATC 298
OY	242	TGCAAATGAACAGCCTGAGAGCTGAGACACGCGTGTGTAATTACTGTGCGAAAAAGAAAG 301
Db	299	TGCAAATGAACAGCCTGAGAGCGCCGAGACACGCGTGTGTAATTACTGTGCGAALACTACAG 358
OY	302	GCTACTGGGGCCAGGAAACCTGTGTACCGTCTCTCA 339
Db	359	ACTACTGGGGCCAGGAAACATGTGTACCGTCTCTCA 396
ID	AAH41661	standard; DNA; 675 BP.
AC	AAH41661;	
DT	28-AUG-2001	(first entry)
XX	DE	Human interleukin 8 antibody nucleotide sequence MI-23H.
KM	XX	Human antibody; detection; Fab; immunoglobulin; heterophilic antibody;
KM	XX	human anti-mouse antibody; HAMA antibody; Interleukin 8; IL-8; Herpes;
KM	XX	targeted antigen; bacterial; fungal; viral; pathogen; human disease;
KM	XX	hepatitis A; hepatitis B; hepatitis C; influenza; Giardia; malaria;
KM	XX	Leishmania; Staphylococcus aureus; Pseudomonas aeruginosa; diagnosis; ds.
OS	XX	Homo sapiens.
OS	XX	Synthetic.

```

XX FN      WO200140306-A1.
XX PD      07-JUN-2001.
XX PF      06-DEC-2000; 2000WO-US033042.
XX PR      06-DEC-1999; 99US-00456090.
XX XX      (BIOS-) BIOSITE DIAGNOSTICS INC.
XX PA      (GENP-) GENPHARM INT.
XX PI      Buechler J, Valkirs G, Gray J, Lonberg N;
XX DR      WPI; 2001-374798/39.
XX PT      Detecting analyte in human sample containing human antibodies binding to
XX PR      nonhuman-antibodies, involves contacting sample with human antibody which
XX XX      binds to antibodies from nonhuman species and detecting binding.
XX
XX PS      Example 22; Page 88; 135bp; English.
XX
XX CC      The present invention describes a method for detecting an analyte in a
XX CC      human sample containing human antibodies that specifically bind to
XX CC      antibodies from a nonhuman species. The method involves contacting the
XX CC      sample with a human antibody (I) which specifically binds to antibodies
XX CC      from a nonhuman species and detecting the binding between (I) and the
XX CC      analyte to indicate presence of the analyte. The method is used for
XX CC      detecting an analyte in a human sample containing human anti-mouse
XX CC      antibody (HMA) (preferably human anti-mouse idotype antibodies and/or
XX CC      heterophilic antibodies). The method can also be used for detecting any
XX CC      type of target antigen including bacterial, fungal and viral pathogens
XX CC      that cause human diseases e.g., hepatitis (A, B and C), influenza, Herpes,
XX CC      Glaridia, Malaria, Leishmania, Staphylococcus aureus, Pseudomonas
XX CC      aeruginosa. Human antibodies can be used as detection reagents for
XX CC      performing clinical diagnostic tests and for performing other in vitro
XX CC      detection assays, including for research purposes. (I) can be used in
XX CC      qualitative assays designed to indicate the presence of one or more
XX CC      target antigens above minimally detectable amounts of antigen in the
XX CC      sample that usually correspond to the sensitivity limitations of the
XX CC      assays for each target antigen. Also, (I) is used to determine the amount
XX CC      of target antigen in a sample in a semi-quantitative or relative sense.
XX CC      Quantification of one or more target antigens in a sample can also be
XX CC      carried out using (I). AAH41612 to AAH41686, and AAB9361 to AAB9399;
XX CC      represent sequences used in the exemplification of the present invention
XX XX
XX SQ      Sequence 675 BP; 151 A; 211 C; 188 G; 125 T; 0 U; 0 Other;
XX
XX Query Match      78.1%; Score 220.4; DB 4; Length 675;
XX Best Local Similarity 87.4%; Pred. No. 7.4e-76;
XX Matches 334; Conservative 0; Mismatches 36; Indels 12; Gaps 1
XX
XX QY      2 AGGTGCACCTGCTCAGTCTGGGGGAGTGTGTTGTTACAGCGTGGGGGTCCTGAGACTCT 61
XX DB      2 AGGTGCACCTGCTGAGTCTGGGGGAGGCGGTGTGTCAGCGTGGAGTCTCTGAGACTCT 61
XX
XX QY      62 CCTGTGACGCTCTGGATTACCTTTGATGATTATGCCATGCACTGGGTCCGACGACTC 121
XX DB      62 CCTGTGACGCGTCTGGATTACCTTCAGTTAATTATGACATGCACTGGGTCCGACGACTC 121
XX
XX QY      122 CAGGCAAGGGGCTGGAGTGGGTGGGAGTATATCATATGATGGAAGTAAATAACTATG 181
XX DB      122 CAGGCAAGGGGCTGGAGTGGGTGGGAGCTATATGATGATGGAAGTAAACCTAACATG 181
XX
XX QY      182 CAGACTCCGTGAAGGGCGGATTACCAATCTCCAGAGACAAATTCGAAGAACACGCTGATC 241
XX DB      182 CAGACTCCGTGAAGGGCGGATTACCAATCTCCAGAGACAAATTCGAAGAACACGCTGATC 241
XX
XX QY      242 TGCAATGAACAGCTGAGAGCTGAGACACGCGCTGTGTATTACTGTGCGAAAGG--- 298
XX DB      242 TGCAATGAACAGCTGAGAGCTGAGACACGCGCTGTGTATTACTGTGCGAAGAGTGGGA 301
XX
XX QY      299 -----MAGCTACTGGGGCCAGGGAACCTTGATCACCGTCTCTCAAGACCCACCA 349
XX

```


Db	362	AGGCCCATCGGCTTCCCT 383
RESULT 8		
AAH30003		
ID	AAH30003	standard, DNA, 675 BP.
XX	AAH30003;	
AC	19-JUL-2001	(first entry)
DT	Anti-IL8 monoclonal antibody nucleotide fragment M1-5H.	
DE	Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;	
KW	human antibody phage display library; immunisation; transgenic animal;	
KW	ds.	
XX	Homo sapiens.	
OS	Synthetic.	
XX	WO200125492-A1.	
PN	12-APR-2001.	
PD	02-OCT-2000; 2000WO-US027237.	
XX	02-OCT-1999; 99US-0157415P.	
XX	01-DEC-1999; 99US-00453234.	
PR	(BIOS-) BIOSITE DIAGNOSTICS INC.	
PA	(GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.	
XX	Buechler J, Valkirs G, Gray J, Lonberg N;	
XX	WPI; 2001-335567/35.	
DR	Producing a human antibody phage display library comprises providing a	
XX	transgenic animal whose genome comprises human immunoglobulin genes and	
PT	isolating nucleic acids encoding antibody chains from lymphatic cells.	
XX	Example 22; Page 91; 161pp; English.	
PS	The present invention describes a method (M1) for producing a human	
XX	antibody phage display library (I), comprising: (1) providing a nonhuman	
CC	transgenic animal (II) whose genome comprises human immunoglobulin genes;	
CC	(2) isolating nucleic acids encoding human antibody chains (III) from	
CC	lymphatic cells; and (3) forming a library of display packages whose	
CC	members comprise a nucleic acid encoding (III) which is displayed from	
CC	the package. The method is used for producing a human antibody display	
CC	library, e.g., a phage display library. The display method may be	
CC	used to screen nucleic acids encoding antibody chains obtained from	
CC	immunised nonhuman transgenic animals, and from this a population of	
CC	antibodies may be prepared. Production of a human monoclonal antibodies	
CC	display library using this method means there is no need to immunise	
CC	humans with antisens, and the difficulties faced with immortalising B	
CC	cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056	
CC	represent sequences used in the exemplification of the present invention	
XX	Sequence 675 BP; 150 A; 210 C; 186 G; 129 T; 0 U; 0 Other;	
SO	Query Match 77.6%; Score 288.8; DB 4; Length 675;	
	Best Local Similarity 87.2%; Pred. No. 2.2e-75;	
	Matches 333; Conservative 0; Mismatches 37; Indels 12; Gaps 1	
QY	2 AGTGCACCTGCTCGAGTGTGGGGAGTGTGTGACAGCGTGGGGGTCCTGAGACTCT 61	
Db	2 AGTGCACGTGTGAGTGTGGGGAGGGGTGTTCAGCTTGGAGTCTTGTGAGACTCT 61	
QY	62 CCTGTGACAGCCTTGGATTCACTTGTGATGATTATGCCATGCACTGGGTCCGACAGCTC 121	
Db	62 CCTGTGACAGCGTGTGATTTCACCTTCAGTTACTATGATGCACTGACCTGGGTCCGACAGCTC 121	
QY	122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAGTAATTAATCTATG 181	

Dd		122	CAGGCAAGGGGCTGGAGTGGGTGAACATTATTAACCTAATGATGGAGATAATTAATCATATG	181
Oy		182	CAAACTTCGGTGAAAGGGCCGATTCACCATCTCCAGAGCAAAATTCGAAGAAGCGGTATC	241
Dd		182	CAACACTCCGGTGAAGGGCCGATTCACCATCTCCAGAGCAAAATTCGAAGAAGCGGTATC	241
Oy		242	TGCMAATGAAACAGCCTGAGAGCTGAGACAACAGCGCTGTATTAATCTGTGCCAAAAG---	298
Dd		242	TGCMAATGAAACAGCCTGAGAGCTGAGAGCAACAGCGCTGTATTAATCTGTGCCAAAAG---	301
Oy		299	-----AAGGCTACTGGGGCCGAGGGAACCTTGATACCTCTCCTCAGACCCACCA	349
Dd		302	TCGGGTACTTTGACTATATGGGGCCGAGGGAACCTTGATACCTCTCCTCAGACCCACCA	361
Oy		350	AGGCTCCGGATGATGTTCCCTCT	371
Dd		362	AGGCCCCATCGCTTCCCTCT	383
RESULT 9				
AAH30019				
ID	AAH30019	standard; DNA; 675 BP.		
Xx		AAH30019;		
Dt		19-JUL-2001 (first entry)		
Xx				
De		Anti-IL8 monoclonal antibody nucleotide fragment M2-11H.		
Xx				
Kw		Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen.		
Km		human antibody phage display library; Immunisation; transgenic animal;		
Rv		ds.		
Os		Homo sapiens.		
Xs		Synthetic.		
Xx				
Pn		MO200125492-A1.		
Pd		12-APR-2001.		
Pf		02-OCT-2000; 2000MO-USO27237.		
Pf				
Pr		02-OCT-1999; 99US-015741SP.		
Pr		01-DEC-1999; 99US-00453234.		
Pa	(BIOS-) BIOSITE DIAGNOSTICS INC.			
Pa	(GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.			
Xx				
Pl	Buechler J, Valkirs G, Gray J, Lonberg N.			
Xx				
Dr	WPI; 2001-335567/35.			
Xx				
Pt	Producing a human antibody phage display library comprises providing a			
Pt	transgenic animal whose genome comprises human immunoglobulin genes and			
Pt	isolating nucleic acids encoding antibody chains from lymphatic cells.			
Xx				
Ps	Example 22; Page 94-95; 161pp; English.			
Xx				
Cc	The present invention describes a method (M1) for producing a nonhan			
Cc	antibody phage display library (I), comprising: (1) providing a nonhan			
Cc	transgenic animal (II) whose genome comprises human immunoglobulin genes;			
Cc	(2) isolating nucleic acids encoding human antibody chains (III) from			
Cc	lymphatic cells; and (3) forming a library of display packages whose			
Cc	members comprise a nucleic acid encoding (III) which is displayed from			
Cc	the package. The method is used for producing a human antibody display			
Cc	library, e.g., a Fab phage display library. The display method may be			
Cc	used to screen nucleic acids encoding antibody chains obtained from			
Cc	immunised nonhan transgenic animals, and from this a population of			
Cc	antibodies may be prepared. Production of a human monoclonal antibodies			
Cc	display library using this method means there is no need to immunise			
Cc	humans with antigens, and the difficulties faced with immortalising B			
Cc	cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056			

CC represent sequences used in the exemplification of the present invention
XX Sequence 675 BP; 150 A; 210 C; 186 G; 129 T; 0 U; 0 Other;
SQ

Query Match 77.6%; Score 288.8; DB 4; Length 675;
Best Local Similarity 87.2%; Pred. No. 2,2e-75;
Matches 333; Conservative 0; Mismatches 37; Indels 12; Gaps 1;

QY 2 AGGTGAGCTGCTGAGTCTGGGGAGTCTGTGTACAGCTGGGGGGTCCGTGAGCTT 61
DB 2 AGGTGAGCTGCTGAGTCTGGGGAGTCTGTGTACAGCTGGGGGGTCCGTGAGCTT 61
QY 62 CCGTGTACAGCTGCTGAGTCTGGGGAGTCTGTGTACAGCTGGGGGGTCCGTGAGCTT 121
DB 62 CCGTGTACAGCTGCTGAGTCTGGGGAGTCTGTGTACAGCTGGGGGGTCCGTGAGCTT 121
QY 122 CAGGCAAGGGGCTGAGTGGGTGGAGTATATCATATGATGAGTAATTAATTAATG 181
DB 122 CAGGCAAGGGGCTGAGTGGGTGGAGTATATCATATGATGAGTAATTAATTAATG 181
QY 182 CAGACTCCGTGAAGGGCCGATTACCACTTCCAGAGCAATTCGAAGAACCGCTGTATC 241
DB 182 CAGACTCCGTGAAGGGCCGATTACCACTTCCAGAGCAATTCGAAGAACCGCTGTATC 241
QY 242 TGCATAATGAACAGCTGAGAGTCAAGGAGTGTGTATTAATGTCGGAAGAAAG--- 298
DB 242 TGCATAATGAACAGCTGAGAGTCAAGGAGTGTGTATTAATGTCGGAAGAGCGGA 301
QY 299 -----AAGGCTACTGGGGCCAGGAAACCTGTGTACAGCTGCTCCTGAGACCCAG 349
DB 302 TGGGTAATCTTTGACTATTTGGGGCCAGGAAACCTGTGTACAGCTGCTCCTGAGAC 361
QY 350 AAGGCTCCGATGTGTTCCTCT 371
DB 362 AAGGCTCCATCGTCTTCCCT 383

RESULT 10
AAH41655
ID AAH41655 standard; DNA; 677 BP.
XX
AC AAH41655;
XX
DT 28-AUG-2001 (first entry)
XX
DE Human interleukin 8 antibody nucleotide sequence M1-3H.
XX
KW Human antibody; detection; Fab; immunoglobulin; heterophilic antibody;
KW human anti-mouse antibody; HAMA antibody; interleukin 8; IL-8; Herpes;
KW target antigen; bacterial; fungal; viral; pathogen; human disease;
KW hepatitis A; hepatitis B; hepatitis C; influenza; Giardia; Malaria;
KW Leishmania; Staphylococcus aureus; Pseudomonas aeruginosa; diagnosis; ds.
OS Homo sapiens.
OS Synthetic.
XX
XX WO200140306-A1.
XX
XX 07-JUN-2001.
XX
XX 06-DEC-2000; 2000WO-US033042.
XX
XX 06-DEC-1999; 99US-00456090.
XX
XX (BIOS-) BIOSITE DIAGNOSTICS INC.
XX (GENP-) GENPHARM INT.
XX
XX Buechler J, Valkirs G, Gray J, Lonberg N;
XX
XX WPI; 2001-374798/39.
XX
XX Detecting analyte in human sample containing human antibodies binding to
PT nonhuman-antibodies, involves contacting sample with human antibody which

PT binds to antibodies from nonhuman species and detecting binding.
XX
XX Example 22; Page 87; 135pp; English.
PS
XX

The present invention describes a method for detecting an analyte in a
CC human sample containing human antibodies that specifically bind to
CC antibodies from a nonhuman species. The method involves contacting the
CC sample with a human antibody (I) which specifically binds to antibodies
CC from a nonhuman species and detecting the binding between (I) and the
CC analyte to indicate presence of the analyte. The method is used for
CC detecting an analyte in a human sample containing human anti-mouse
CC antibody (HAMA) (preferably human anti-mouse idiotype antibodies and/or
CC heterophilic antibodies). The method can also be used for detecting any
CC type of target antigen including bacterial, fungal and viral pathogens
CC that cause human diseases e.g., hepatitis (A,B and C), influenza, Herpes,
CC Giardia, Malaria, Leishmania, Staphylococcus aureus, Pseudomonas
CC aeruginosa. Human antibodies can be used as detection reagents for
CC performing clinical diagnostic tests and for performing other in vitro
CC detection assays, including for research purposes. (I) can be used in
CC qualitative assays designed to indicate the presence of one or more
CC target antigens above minimally detectable amounts of antigen in the
CC sample that usually correspond to the sensitivity limitations of the
CC assays for each target antigen. Also, (I) is used to determine the amount
CC of target antigen in a sample in a semi-quantitative or relative sense.
CC Quantification of one or more target antigens in a sample can also be
CC carried out using (I). AAH41612 to AAH41686, and AAB93961 to AAB93999,
CC represent sequences used in the exemplification of the present invention
XX

SQ Sequence 677 BP; 150 A; 213 C; 185 G; 129 T; 0 U; 0 Other;
Query Match 77.5%; Score 288.2; DB 4; Length 677;
Best Local Similarity 86.9%; Pred. No. 3.3e-75;
Matches 333; Conservative 0; Mismatches 38; Indels 12; Gaps 1;

QY 1 GAGGTGAGCTGCTGAGTCTGGGGAGTCTGTGTACAGCTGGGGGGTCCGTGAGACTC 60
DB 3 GAGTGTACAGCTGCTGAGTCTGGGGAGTCTGTGTACAGCTGGGGGGTCCGTGAGACTC 62
QY 61 TCCTGTGAGCTCTGTGATTCACCTTTGATGATTAATGATGATGATGATGATGATGAT 120
DB 63 TCCTGTGAGCTCTGTGATTCACCTTTGATGATTAATGATGATGATGATGATGATGAT 122
QY 121 CCAAGCAAGGGGCTGAGTGGGTGGAGTATATCATATGATGAGTAATTAATTAATCTAT 180
DB 123 CCAAGCAAGGGGCTGAGTGGGTGGAGTATATCATATGATGAGTAATTAATTAATCTAT 182
QY 181 GCAGACTCCGTGAAGGGCCGATTACCACTTCCAGAGCAATTCGAAGAACCGCTGTAT 240
DB 183 GCAGACTCCGTGAAGGGCCGATTACCACTTCCAGAGCAATTCGAAGAACCGCTGTAT 242
QY 241 CTGCAATGAACAGCTGAGAGTGAAGACAGCGCTGTGTATTAATGTCGGAAGAAAG-- 298
DB 243 CTGCAATGAACAGCTGAGAGTGAAGACAGCGCTGTGTATTAATGTCGGAAGAGCGGG 302
QY 299 -----AAGGCTACTGGGGCCAGGAAACCTGTGTACAGCTGCTCCTGAGACCCAG 348
DB 303 ATCGGTAATCTTTGACTATTTGGGGCCAGGAAACCTGTGTACAGCTGCTCCTGAGAC 362
QY 349 AAGGCTCCGATGTGTTCCTCT 371
DB 363 AAGGCTCCATCGTCTTCCCT 385

RESULT 11
AAH30001
ID AAH30001 standard; DNA; 677 BP.
XX
AC AAH30001;
XX
XX 19-JUL-2001 (first entry)
XX
XX Anti-IL8 monoclonal antibody nucleotide fragment M1-3H.
XX
XX


```
QY 122 CAGCAAGGGGCTGAGTGGGGTGCAGTTATCATATGATGAGAAATAAATACATG 181
DB 179 CAGGCAAGGGGCTGAGTGGGGTGCAGTTATGATGATGAGAAATAAATACATG 238
QY 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAACACCGCTGATC 241
DB 239 CAAACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAACACCGCTGATC 298
QY 242 TGCAAATGAACAGCTGAGAGCTGAGAGACACGGCTGTGATTACTGTGCGAAAAAGAG 301
DB 299 TGCAAATGAACAGCTGAGAGCTGAGAGACACGGCTGTGATTACTGTGCGAGATGGGG 358
QY 302 G-----CTACTGGGGCCAGGGAACCTGTGTACCGTCTCCCTCAG 340
DB 359 GTAAAGCAGTGCCTGTCTGACTACTGAGGGCCAGGGAATCTGTGTACCGTCTCCCTCAG 418
QY 341 CACCCACCAAGGCTCCGATGTGTCCTCT 371
DB 419 CCTCCACCAAGGGCCATCGTCTTCCCTCT 449

RESULT 13
AAA46870
ID AAA46870 standard; DNA; 1392 BP.
XX
AC AAA46870;
XX
DT 03-OCT-2000 (first entry)
XX
DE DNA encoding the heavy chain of immunoglobulin clone 6.1.1.
XX
KM Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
KW proliferative disorder; cancer; immunodeficient disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1392
FT /tag= a
XX
PN WO200037504-A2.
XX
PD 29-JUN-2000.
XX
PF 23-DEC-1999; 99MO-US030895.
XX
PR 23-DEC-1998; 98US-0113647P.
XX
PA (PFIZ ) PFIZER INC.
PA (ABGE-) ABGENIX INC.
XX
PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
PI Corvalan JR;
XX
DR MPI, 2000-442647/38.
DR P-PSDB; AAY93707.
XX
PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
PT -4 containing specified heavy and light chain sequences, useful for
PT treating, e.g. immune disorders.
XX
PS Example 2; Fig 1D; 157bp; English.
XX
CC The present sequence encodes a heavy chain of an antibody of the
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
CC -4. Antibodies of the invention are composed of a heavy chain variable
CC region, comprising a modified contiguous sequence from a P1-PR3 sequence
CC encoded by a human VH3-33 family gene. The modifications are contained in
CC CDR1, CDR2 and/or framework regions. The antibodies may be used to
CC inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
CC disorders (e.g. autoimmune disease, diabetes and graft rejection) and
CC proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
```

```
CC used to up-regulate immune system to up-regulate immunodeficient
CC disorders
XX
SQ Sequence 1392 BP; 314 A; 432 C; 391 G; 255 T; 0 U; 0 Other;
Query Match 77.3%; Score 287.4; DB 3; Length 1392;
Best Local Similarity 86.8%; Pred. No. 7.3e-75;
Matches 334; Conservative 0; Mismatches 36; Indels 15; Gaps 1;

QY 2 AGGTGAGCTGCTCGAGTCTGGGGAGTGTGTATACAGCTGGGGGCTCCAGACTCT 61
DB 59 AGGTGAGCTGCTGAGTCTGGGGAGGCGTGTGTATACAGCTGGGGGCTCCAGACTCT 118
QY 62 CCTGTGACGCTTGTGATTCACCTTGAATGATATGCACTGCGGCTCCAGGCTC 121
DB 119 CCTGTGACGCTTGTGATTCACCTTGAATGATATGCACTGCGGCTCCAGGCTC 178
QY 122 CAGCAAGGGGCTGAGTGGGGTGCAGTTATCATATGATGAGAAATAAATACATG 181
DB 179 CAGGCAAGGGGCTGAGTGGGGTGCAGTTATGATGATGAGAAATAAATACATG 238
QY 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAACACCGCTGATC 241
DB 239 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAACACCGCTGATC 298
QY 242 TGCAAATGAACAGCTGAGAGCTGAGAGACACGGCTGTGATTACTGTGCGAAAAAGAA- 300
DB 299 TGCAAATGAACAGCTGAGAGCTGAGAGACACGGCTGTGATTACTGTGCGAGGCGGAC 358
QY 301 -----GGCTACTGGGGGCAGGGAACCTGTGTACCGTCTCTCCAGACCCA 346
DB 359 TGTGGGTTACTTGTGACTGTGGGGCCAGGGAACCTGTGTACCGTCTCTCCAGACCCA 418
QY 347 CCAAGGCTCCGATGTGTCCTCT 371
DB 419 CCAAGGGCCATCGTCTTCCCTCT 443

RESULT 14
AAA46896
ID AAA46896 standard; DNA; 1392 BP.
XX
AC AAA46896;
XX
DT 03-OCT-2000 (first entry)
XX
DE DNA encoding the heavy chain of immunoglobulin clone 6.1.1.
XX
KM Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
KW proliferative disorder; cancer; immunodeficient disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1392
FT /tag= a
FT sig_peptide 1..57
FT /tag= b
XX
PN WO200037504-A2.
XX
PD 29-JUN-2000.
XX
PF 23-DEC-1999; 99MO-US030895.
XX
PR 23-DEC-1998; 98US-0113647P.
XX
PA (PFIZ ) PFIZER INC.
PA (ABGE-) ABGENIX INC.
XX
PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
PI Corvalan JR;
```

XX WPI; 2000-442647/38.
 DR P-PSDB; AAY93732.
 XX
 PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
 XX -4 containing specified heavy and light chain sequences, useful for
 PT treating, e.g. immune disorders.
 PS
 XX Example 2; Fig 221; 157pp; English.
 XX
 CC The present sequence encodes a heavy chain of an antibody of the
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
 CC -4. Antibodies of the invention are composed of a heavy chain variable
 CC region, comprising a modified contiguous sequence from a F1-F3 sequence
 CC encoded by a human VH3-33 family gene. The modifications are contained in
 CC CDR1, CDR2 and/or framework regions. The antibodies may be used to
 CC inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
 CC disorders (e.g. autoimmune disease, diabetes and graft rejection) and
 CC proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
 CC used to up-regulate immune system to up-regulate immunodeficient
 CC disorders
 CC
 SQ Sequence 1392 BP; 314 A; 432 C; 391 G; 255 T; 0 U; 0 Other;
 XX
 Query Match 77.3%; Score 287.4; DB 3; Length 1392;
 Best Local Similarity 86.8%; Pred. No. 7.3e-75;
 Matches 334; Conservative 0; Mismatches 36; Indels 15; Gaps 1;
 XX
 QY 2 AGGTGACAGTCTCGAGTCTGGGGAGTGTGTGATAGAGCTGGGGGCTCCCTGAGACTCT 61
 DB 59 AGGTGACAGTCTGGAGTCTGGGGAGGCTGTGTGATAGAGCTGGGGAGTCTCCCTGAGACTCT 118
 QY 62 CCTGTGACAGCTCTGATTCACCTTTGATGATTAATCCATGACCTGGTCCGACGCTC 121
 DB 119 CCTGTACAGGCTCTGATTCACCTTCACTGATGATGACATGCTGGTCCGACGCTC 178
 QY 122 CAGGCAAGGGGCTGGAGTGGGTGGGAGTTATATCATATGATGGAATTAATACTATG 181
 DB 179 CAGGCAAGGGGCTGGAGTGGGTGGGAGTTATATGATGGAATTAATACTATG 238
 QY 182 CAGACTCCGTAAGAGGCGGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 241
 DB 239 CAGACTCCGTAAGAGGCGGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 298
 QY 242 TGCATATGAACAGCTGTAGAGTGTAGAGACACGCTGTGATTAATCTGTGCAAAAGAA- 300
 DB 299 TGCATATGAACAGCTGTAGAGTGTAGAGACACGCTGTGATTAATCTGTGCAAGCGGAC 358
 QY 301 -----GGCTACTGAGGGCCAGGGAACCTGGTCAAGCTCTCCCTGAGACCA 346
 DB 359 TGCTGGGTACTTTGACTACTGAGGCGAGGGAACCTGGTCAAGCTCTCCCTGAGACCA 418
 QY 347 CCAAGGCTCCGATGTGTTCCCTCT 371
 DB 419 CCAAGGCGCATGCGTCTTCCCTCT 443
 XX
 RESULT 15
 AAD54347
 ID AAD54347 standard; cDNA; 1392 BP.
 XX
 AC AAD54347;
 XX
 DT 17-JUN-2003 (first entry)
 XX
 DE Human 6.1.1 anti-CTLA-4 antibody heavy chain cDNA.
 XX
 KW Human; cytotoxic T lymphocyte antigen-4; therapy; CTLA-4 antibody;
 XX cancer; gene; ss.
 OS Homo sapiens.
 XX
 Key Location/Qualifiers
 FH

FT CDS 1..1392
 FT /*tag= a
 FT /product= "Anti-CTLA-4 antibody heavy chain"
 FT sig_peptide 1..57
 FT /*tag= b
 FT mat_peptide 58..1389
 FT /*tag= c
 FT /product= "Mature anti-CTLA-4 antibody heavy chain"
 XX
 XX EPI262193-A1.
 XX
 XX PD 04-DEC-2002.
 XX
 XX 23-MAY-2002; 2002EP-00253652.
 XX
 XX 23-MAY-2001; 2001US-0293042P.
 XX
 XX (Pfizer) Pfizer Prod Inc.
 XX
 XX PI Hanson DC, Mueller EE;
 XX
 XX WPI; 2003-131215/13.
 DR P-PSDB; AAE35887.
 XX
 XX Use of human anti-cytotoxic T lymphocyte antigen-4 antibody in the
 PT preparation of medicament for the treatment of cancer.
 XX
 XX Disclosure; Fig 1L; 76pp; English.
 XX
 CC The invention relates to the use of human anti-cytotoxic T lymphocyte
 CC antigen-4 (anti-CTLA-4) antibody in the preparation of a medicament for
 CC the treatment of cancer such as bone cancer, pancreatic cancer, skin
 CC cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian
 CC cancer, cancer of the anal region, stomach cancer, breast cancer,
 CC testicular cancer, uterine cancer and carcinoma of the fallopian tubes.
 CC The present sequence is human anti-CTLA-4 antibody heavy chain cDNA
 CC
 SQ Sequence 1392 BP; 314 A; 432 C; 391 G; 255 T; 0 U; 0 Other;
 XX
 Query Match 77.3%; Score 287.4; DB 10; Length 1392;
 Best Local Similarity 86.8%; Pred. No. 7.3e-75;
 Matches 334; Conservative 0; Mismatches 36; Indels 15; Gaps 1;
 XX
 QY 2 AGGTGACAGTCTCGAGTCTGGGGAGTGTGTGATAGAGCTGGGGGCTCCCTGAGACTCT 61
 DB 59 AGGTGACAGTCTGGAGTCTGGGGAGGCTGTGTGATAGAGCTGGGGAGTCTCCCTGAGACTCT 118
 QY 62 CCTGTGACAGCTCTGATTCACCTTTGATGATTAATCCATGACCTGGTCCGACGCTC 121
 DB 119 CCTGTACAGGCTCTGATTCACCTTCACTGATGATGACATGCTGGTCCGACGCTC 178
 QY 122 CAGGCAAGGGGCTGGAGTGGGTGGGAGTTATATCATATGATGGAATTAATACTATG 181
 DB 179 CAGGCAAGGGGCTGGAGTGGGTGGGAGTTATATGATGGAATTAATACTATG 238
 QY 182 CAGACTCCGTAAGAGGCGGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 241
 DB 239 CAGACTCCGTAAGAGGCGGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 298
 QY 242 TGCATATGAACAGCTGTAGAGTGTAGAGACACGCTGTGATTAATCTGTGCAAAAGAA- 300
 DB 299 TGCATATGAACAGCTGTAGAGTGTAGAGACACGCTGTGATTAATCTGTGCAAGCGGAC 358
 QY 301 -----GGCTACTGAGGGCCAGGGAACCTGGTCAAGCTCTCCCTGAGACCA 346
 DB 359 TGCTGGGTACTTTGACTACTGAGGCGAGGGAACCTGGTCAAGCTCTCCCTGAGACCA 418
 QY 347 CCAAGGCTCCGATGTGTTCCCTCT 371
 DB 419 CCAAGGCGCATGCGTCTTCCCTCT 443
 XX
 Search completed: December 7, 2004, 06:41:27

Tue Dec 7 14:35:57 2004

us-09-403-107-145.rng

Page 11

Job time : 315.933 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 05:42:24 ; Search time 76.8 Seconds
(without alignments)
3442.884 Million cell updates/sec

Title: US-09-403-107-145

Perfect score: 372
Sequence: 1 gagggtgcagctgctgcagtc.....ctccgagatgttccctccta 372

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/prodata/1/ina/5A COMB.seq: *
2: /cgn2_6/prodata/1/ina/5B COMB.seq: *
3: /cgn2_6/prodata/1/ina/6A COMB.seq: *
4: /cgn2_6/prodata/1/ina/6B COMB.seq: *
5: /cgn2_6/prodata/1/ina/6C COMB.seq: *
6: /cgn2_6/prodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	290.4	78.1	675	4	US-09-456-090A-67 Sequence 67, App1
2	290.4	78.1	675	4	US-09-453-234-67 Sequence 67, App1
3	288.8	77.6	675	4	US-09-456-090A-59 Sequence 59, App1
4	288.8	77.6	675	4	US-09-456-090A-91 Sequence 91, App1
5	288.8	77.6	675	4	US-09-453-234-59 Sequence 59, App1
6	288.8	77.6	675	4	US-09-453-234-91 Sequence 91, App1
7	288.2	77.5	677	4	US-09-456-090A-55 Sequence 55, App1
8	288.2	77.5	677	4	US-09-453-234-55 Sequence 55, App1
9	287.4	77.3	1392	4	US-09-472-087-30 Sequence 30, App1
10	287.4	77.3	1392	4	US-09-472-087-59 Sequence 59, App1
11	287.2	77.2	675	4	US-09-456-090A-101 Sequence 101, App1
12	287.2	77.2	675	4	US-09-453-234-101 Sequence 101, App1
13	286	76.9	1395	4	US-09-472-087-28 Sequence 28, App1
14	286	76.9	1395	4	US-09-472-087-57 Sequence 57, App1
15	285.8	76.8	1392	4	US-09-472-087-27 Sequence 27, App1
16	285.8	76.8	1392	4	US-09-472-087-53 Sequence 53, App1
17	285.8	76.8	1392	4	US-09-472-087-55 Sequence 55, App1
18	284.2	76.4	1999	4	US-09-472-087-54 Sequence 54, App1
19	284	76.3	675	4	US-09-456-090A-107 Sequence 107, App1
20	284	76.3	675	4	US-09-453-234-107 Sequence 107, App1
21	282.4	75.9	675	4	US-09-456-090A-99 Sequence 99, App1
22	282.4	75.9	675	4	US-09-456-090A-105 Sequence 105, App1
23	282.4	75.9	675	4	US-09-456-090A-109 Sequence 109, App1
24	282.4	75.9	675	4	US-09-453-234-99 Sequence 99, App1
25	282.4	75.9	675	4	US-09-453-234-105 Sequence 105, App1
26	282.4	75.9	675	4	US-09-453-234-109 Sequence 109, App1
27	281.8	75.8	675	4	US-09-456-090A-93 Sequence 93, App1

28	281.8	75.8	675	4	US-09-453-234-93	Sequence 93, App1
29	279.2	75.1	675	4	US-09-456-090A-57	Sequence 57, App1
30	279.2	75.1	675	4	US-09-456-090A-61	Sequence 61, App1
31	279.2	75.1	675	4	US-09-453-234-57	Sequence 57, App1
32	279.2	75.1	675	4	US-09-453-234-61	Sequence 61, App1
33	278.2	74.8	5925	4	US-09-415-926A-78	Sequence 78, App1
34	277.6	74.6	675	4	US-09-456-090A-69	Sequence 69, App1
35	277.6	74.6	675	4	US-09-453-234-69	Sequence 69, App1
36	276	74.2	675	4	US-09-456-090A-65	Sequence 65, App1
37	276	74.2	675	4	US-09-456-090A-95	Sequence 95, App1
38	276	74.2	675	4	US-09-456-090A-97	Sequence 97, App1
39	276	74.2	675	4	US-09-453-234-95	Sequence 95, App1
40	276	74.2	675	4	US-09-453-234-97	Sequence 97, App1
41	276	74.2	675	4	US-09-453-234-97	Sequence 97, App1
42	274.4	73.8	675	4	US-09-456-090A-53	Sequence 53, App1
43	274.4	73.8	675	4	US-09-453-234-53	Sequence 53, App1
44	273.6	73.5	369	4	US-09-560-198A-9	Sequence 9, App1
45	272.8	73.3	512	3	US-08-545-809A-30	Sequence 30, App1

ALIGNMENTS

```
RESULT 1
US-09-456-090A-67
Sequence 67, Application US/09456090A
Patent No. 6680209
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Walkiers, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lomborg, Nils
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERENCE: 020015-000200US
CURRENT APPLICATION NUMBER: US/09/456,090A
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 67
LENGTH: 675
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(675)
OTHER INFORMATION: M1-23H
US-09-456-090A-67

Query Match      78.1%; Score 290.4; DB 4; Length 675;
Best Local Similarity 87.4%; Pred. No. 1,6e-85;
Matches 334; Conservative 0; Mismatches 36; Indels 12; Gaps 1;

QY      2 AGGTGAGCTGCTCGAGTCTGGGGAGTGTGTGTAACAGCTGGGGGCTCCAGACTCT 61
        |||||
DB      2 AGGTGAGCTGCTCGAGTCTGGGGAGTGTGTGTAACAGCTGGGGGCTCCAGACTCT 61
        |||||

QY      62 CCTGTGACCTCTGTGATTCACCTTGATGATTATGATTCAGTGGTCCGACAGCTC 121
        |||||
DB      62 CCTGTGACCTCTGTGATTCACCTTGATGATTATGATTCAGTGGTCCGACAGCTC 121
        |||||

QY      122 CAGGCAAGGGCTGTGAGTGTGGTGTGATTCATATGATGAGAACTAATAATATATG 181
        |||||
DB      122 CAGGCAAGGGCTGTGAGTGTGGTGTGATTCATATGATGAGAACTAATAATAATATG 181
        |||||

QY      182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGAACCGCTGTATC 241
        |||||
DB      182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGAACCGCTGTATC 241
        |||||

QY      242 TGCATATGAACAGCTGTGAGAGTGTGAGAGACAGGCTGTGTATTAATGCGGAAAAGG--- 298
        |||||
DB      242 TGCATATGAACAGCTGTGAGAGTGTGAGAGACAGGCTGTGTGTATTAATGCGGAAAAGG 301
        |||||

QY      299 -----AAGCTACTGGGGCCAGAGGAACCTGTGTACCGTCTCTCAGACCAACCA 349
```


[illegible]

RESULT 2
US-09-453-234-67

```

1      Sequence 67, Application US/09453234
2      Patent No.6794112
3      GENERAL INFORMATION:
4      APPLICANT: Beechler, Joe
5      APPLICANT: Valktirs, Gunars
6      APPLICANT: Gray, Jeff
7      APPLICANT: Lomborg, Nils
8      APPLICANT: Biostate Diagnostics, Inc.
9      APPLICANT: Genpharm International
10     TITLE OF INVENTION: Human Antibodies
11     FILE REFERENCE: 020015-000110US
12     CURRENT APPLICATION NUMBER: US/09/453,234
13     CURRENT FILING DATE: 1999-12-01
14     PRIOR APPLICATION NUMBER: US 60/157,415
15     PRIOR FILING DATE: 1999-10-02
16     NUMBER OF SEQ ID NOS: 112
17     SOFTWARE: PatentIn Ver. 2.1
18     SEQ ID NO 67
19     LENGTH: 675
20     TYPE: DNA
21     ORGANISM: Homo sapiens
22     FEATURE:
23     OTHER INFORMATION: M1-23H
24     NAME/KEY: CDS
25     LOCATION: (1) .. (675)
26     US-09-453-234-67

```

Query Match	78.1%	Score 290.4	DB 4	Length 675

Best Local Similarity 87.4%; Pred. NO. 16e-85;
Matches 334; Conservative 0; Mismatches 36; Indels 12; Gaps 1

QY	2	AGGTGCAGAGCTGCTGAACTCTGGGGGAAAGTCGTGGTA	CAGCGCTGGGGGGTCCCTGAGACTCT	61
Db	2	AGGTGCAGAGCTGCTGAACTCTGGGGGAAAGTCGTGGTA	CAGCGCTGGGGGGTCCCTGAGACTCT	61
QY	62	CCTGTGCAGGCTCTGATTCACCTTTGATGATTAATCCATGCAC	TGTGCGCCAGGCTC	122
Db	62	CCTGTGCAGGCTCTGATTCACCTTTGATGATTAATCCATGCAC	TGTGCGCGCCAGGCTC	122
QY	122	CAGGCAAGGGGCTTGGATGTGGGTGGCAGTTATATCATATGATGGAAGTAAATTAATCTATG		182
Db	122	CAGGCAAGGGGCTTGGATGTGGGTGGCAGTTATATGATGATGGAAGTAAATTAATCTATG		182
QY	182	CAGACTCCGTGGAAGGGGCGAATTCACCAATTCACGAGACAATTC	CAAGAAACAGCGCTGATC	242
Db	182	CAGACTCCGTGGAAGGGGCGAATTCACCAATTCACGAGACAATTC	CAAGAAACAGCGCTGATC	242
QY	242	TGCAAAATGAACAGCGCTGAGAGCTGAGAGCA	CGGCTGTGTATTA	CTGTGCGAAAAAG--- 299
Db	242	TGCAAAATGAACAGCGCTGAGAGCTGAGAGCA	CGGCTGTGTATTA	CTGTGCGAAGATGGGA 302
QY	299	-----AAGGCTACTGCGGGCCAGGGAA	CCTGTGTACCGTCTCTCAGACCCACCA	342
Db	302	TAGGCTACTTTGACTACTGCGGGCCAGGGAA	CCTGTGTACCGTCTCTCAGACTTCACCA	362
QY	350	AGGCTCGAGATGTGTCCCTCT	371	
Db	362	AGGCGCATGTGCTCTTCCCCCT	383	

RESULT 3
US-09-456-090A-59
; Sequence 59, Application US/09456090A

```

Patent No. 6680209
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lomborg, Nils
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERENCE: 020015-000200US
CURRENT APPLICATION NUMBER: US/09/456,090A
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ. ID NOS: 110
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 58
LENGTH: 675
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(675)
OTHER INFORMATION: M1-5H
US-09-456-090A-59

```

Query Match	77.6%	Score 288.8;	DB 4;	Length 675;
Best Local Similarity	87.2%;	Pred. No. 5.4e-85;		
Matches 333;	Conservative	0;	Mismatches 37;	Indels 12;
				Gaps 1

Oy	AGGTGAGCTGCTCCAGATCTGGGGGAGTCTGTGTAACAGCTGGGGGGTCTCCTAGACTCT	61
Oy	AGGTGAGCTGCTCCAGATCTGGGGGAGTCTGTGTAACAGCTGGGGGGTCTCCTAGACTCT	61
Db	2 AGGTGAGCTGCTGGAGTCTGGGGGAGGCGTGTCTCAAGCTGGGAGGTCCTTAGACTCT	61
Oy	62 CCTGTGACGCTCTGGATTCACTTTGATGATATGCAATGCACTGGAGTCCGCGACGCT	121
Db	62 CCTGTGACGCTCTGGATTCACTTTGATGATATGCAATGCACTGGAGTCCGCGACGCT	121
Oy	122 CAGGCAAGGGGCTGGAGTGGGTGGGAGTTATATCATATGATGGAAGTAATTAATTAATG	181
Db	122 CAGGCAAGGGGCTGGAGTGGGTGGGAGTTATTAACCTTAATGATGGAGTAATTAATTAATG	181
Oy	182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCGAAGAACACGCTGTATC	241
Db	182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCGAAGAACACGCTGTATC	241
Oy	242 TGCATAATGAAACAGCTGAGAGCTGAGACAACGGCTGTGTATTAATGTTGCGAAAAAGG--	298
Db	242 TGCATAATGAAACAGCTGAGAGCTGAGACAACGGCTGTGTATTAATGTTGCGAAAAAGG	301
Oy	299 -----AAGCTTACTGGGGGCTGAGGAACTCTGTGTACCTCTCTCAAGACCCACCA	349
Db	302 TCGGATTAATTTGATTAATGGGGGCTGAGGAACTCTGTGTACCTCTCTCAAGACCCACCA	361
Oy	350 AGGCTCCGAAATGTATCCCTCT 371	
Db	362 AGGAGCCATGCGTCTTCCCTCT 383	

RESULT 4
US-09-456-090A-91

```

/ Sequence 91, Application US/09456090A
/ Patent No. 6680209
/
/ GENERAL INFORMATION:
/
/ APPLICANT: Buechler, Joe
/ APPLICANT: Walkirs, Gunars
/ APPLICANT: Gray, Jeff
/
/ APPLICANT: Lomborg, Nils
/
/ TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
/
/ FILE REFERENCE: 020015-000200US
/
/ CURRENT APPLICATION NUMBER: US/09/456,090A
/
/ CURRENT FILING DATE: 1999-12-06
/
/ NUMBER OF SEQ ID NOS: 110
/
/ SOFTWARE: PatentIn Ver. 2.1
/
/ SEQ ID NO 91
/
/ LENGTH: 675
/
/ TYPE: DNA
/

```

OY		2	AGGTCACAGCTCTCGAGTCTTGGGGGAGTCCGTGTACAGCCTGGGGGGGTCCCTGAGA	61
Dd		2	AGGTGCACCTGTGTGAAGTCTGGGGGAGCGTGTATCAAGCTTGGGAGACTCT	61
OY		62	CCTGTGACGCTCTGTGATTCACTTTGTATGATTAATGCCATGCACTGGGTCCGCAAGCTC	121
Dd		62	CCTGTGACAGCGTCTGGATTATTCCTTCAGTTACTATATGGCATGCACTGGGTCCGCAAGCTC	121
OY		122	CAGGCAGAGGGGCTTGAGTGGGTGGCAGTTATATCATATGATGAAAGTATAATATCTATG	181
Dd		122	CAGGCAGAGGGGCTTGAGTGGGTGGCACATTATACCTTATGATGAGATATATTAATATCTATG	181
OY		182	CAGACTCCGTGTAAGGGCCGATTTCACATCTCCAGAGAACATTCAGAACACGCTGTATC	241
Dd		182	CAGACTCCGTGTAAGGGCCGATTTCACATCTCCAGAGAACATTCAGAACACGCTGTATC	241
OY		242	TGCAAAATGAACAGCCTGTGAGACTGAGACAACGCGTGTGTATTACTGTGTGCAAAAAAG---	298
Dd		242	TGCAAAATGAACAGCCTGTGAGACTGAGACAACGCGTGTGTATTACTGTGTGCAAAAAAG---	298
OY		299	-----AAGCTTACTGGGGCCAGGGAACCTTGTTACCGCTCTCTCAGCACCCACCA	349
Dd		302	TGGGTACTTTGACTATGTGGGGCAGGGAACTTGTTACCGCTCTCTCAGCACCCACCA	361
OY		350	AGGCTCCGGATGTGTCCCTCT	371
Dd		362	AGGGCCATCGGTCTTCCCCCT	383

RESULT 6
US-09-453-234-91
; Sequence 91, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
 APPLICANT: Buechler, Joe
 APPLICANT: Walkiers, Junars
 APPLICANT: Gray, Jeff
 APPLICANT: Lomborg, Nils
 APPLICANT: Biosite Diagnostics, Inc.
 APPLICANT: Genpharm International
 TITLE OF INVENTION: Human Antibodies
 FILE REFERENCE: 020015-000110US
 CURRENT APPLICATION NUMBER: US/09/453,234
 CURRENT FILING DATE: 1999-12-01
 PRIOR APPLICATION NUMBER: US 60/157,415
 PRIOR FILING DATE: 1999-10-02
 NUMBER OF SEQ ID NOS: 112
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 91
 LENGTH: 675
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(675)
 OTHER INFORMATION: M2-11H
US-09-453-234-91

Query Match 77.6%; Score 288.8; DB 4; Length 675;
Best Local Similarity 87.2%; Pred. No. 5,4e-85;
Matches 333; Conservativeness 0; Mismatches 37; Indels 12; Gaps

OY		2	AGGTGCAGCTCTCGAGTCTTGGGGAGTCCGTGTACAGCCTGGGGGGGTCCCTGAGA	61
Dd		2	AGGTGCACCTGTGTGAAGTCTGGGGGAGCGTGTATCAAGCTTGGGAGACTCT	61
OY		62	CCTGTGACGCTCTGTGATTCACTTTGTATGATTAATGCCATGCACTGGGTCCGCAAGCTC	121
Dd		62	CCTGTGACAGCGTCTGGATTATTCCTTCAGTTACTATATGGCATGCACTGGGTCCGCAAGCTC	121
OY		122	CAGGCAGAGGGGCTTGAGTGGGTGGCAGTTATATCATATGATGAAAGTATAATATCTATG	181
Dd		122	CAGGCAGAGGGGCTTGAGTGGGTGGCACATTATACCTTATGATGAGATATATTAATATCTATG	181
OY		182	CAGACTCCGTGTAAGGGCCGATTTCACATCTCCAGAGAACATTCAGAACACGCTGTATC	241
Dd		182	CAGACTCCGTGTAAGGGCCGATTTCACATCTCCAGAGAACATTCAGAACACGCTGTATC	241
OY		242	TGCAAAATGAACAGCCTGTGAGACTGAGACAACGCGTGTGTATTACTGTGTGCAAAAAAG---	298
Dd		242	TGCAAAATGAACAGCCTGTGAGACTGAGACAACGCGTGTGTATTACTGTGTGCAAAAAAG---	298
OY		299	-----AAGCTTACTGGGGCCAGGGAACCTTGTTACCGCTCTCTCAGCACCCACCA	349
Dd		302	TGGGTACTTTGACTATGTGGGGCAGGGAACTTGTTACCGCTCTCTCAGCACCCACCA	361
OY		350	AGGCTCCGGATGTGTCCCTCT	371
Dd		362	AGGGCCATCGGTCTTCCCCCT	383

RESULT 6
US-09-453-234-91
; Sequence 91, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
 APPLICANT: Buechler, Joe
 APPLICANT: Walkiers, Junars
 APPLICANT: Gray, Jeff
 APPLICANT: Lomborg, Nils
 APPLICANT: Biosite Diagnostics, Inc.
 APPLICANT: Genpharm International
 TITLE OF INVENTION: Human Antibodies
 FILE REFERENCE: 020015-000110US
 CURRENT APPLICATION NUMBER: US/09/453,234
 CURRENT FILING DATE: 1999-12-01
 PRIOR APPLICATION NUMBER: US 60/157,415
 PRIOR FILING DATE: 1999-10-02
 NUMBER OF SEQ ID NOS: 112
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 91
 LENGTH: 675
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(675)
 OTHER INFORMATION: M2-11H
US-09-453-234-91

Query Match 77.6%; Score 288.8; DB 4; Length 675;
Best Local Similarity 87.2%; Pred. No. 5,4e-85;
Matches 333; Conservativeness 0; Mismatches 37; Indels 12; Gaps

OY		2	AGGTGCAGCTCTCGAGTCTTGGGGAGTCCGTGTACAGCCTGGGGGGGTCCCTGAGA	61
Dd		2	AGGTGCACCTGTGTGAAGTCTGGGGGAGCGTGTATCAAGCTTGGGAGACTCT	61
OY		62	CCTGTGACGCTCTGTGATTCACTTTGTATGATTAATGCCATGCACTGGGTCCGCAAGCTC	121
Dd		62	CCTGTGACAGCGTCTGGATTATTCCTTCAGTTACTATATGGCATGCACTGGGTCCGCAAGCTC	121
OY		122	CAGGCAGAGGGGCTTGAGTGGGTGGCAGTTATATCATATGATGAAAGTATAATATCTATG	181
Dd		122	CAGGCAGAGGGGCTTGAGTGGGTGGCACATTATACCTTATGATGAGATATATTAATATCTATG	181
OY		182	CAGACTCCGTGTAAGGGCCGATTTCACATCTCCAGAGAACATTCAGAACACGCTGTATC	241
Dd		182	CAGACTCCGTGTAAGGGCCGATTTCACATCTCCAGAGAACATTCAGAACACGCTGTATC	241
OY		242	TGCAAAATGAACAGCCTGTGAGACTGAGACAACGCGTGTGTATTACTGTGTGCAAAAAAG---	298
Dd		242	TGCAAAATGAACAGCCTGTGAGACTGAGACAACGCGTGTGTATTACTGTGTGCAAAAAAG---	298
OY		299	-----AAGCTTACTGGGGCCAGGGAACCTTGTTACCGCTCTCTCAGCACCCACCA	349
Dd		302	TGGGTACTTTGACTATGTGGGGCAGGGAACTTGTTACCGCTCTCTCAGCACCCACCA	361
OY		350	AGGCTCCGGATGTGTCCCTCT	371
Dd		362	AGGGCCATCGGTCTTCCCCCT	383


```
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GITMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
FILE REFERENCE: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 30
LENGTH: 1392
TYPE: DNA
ORGANISM: Homo sapiens
US-09-472-087-30

Query Match
Best Local Similarity 77.3%; Score 287.4; DB 4; Length 1392;
Matches 334; Conservative 0; Mismatches 36; Indels 15; Gaps 1;

QY 2 AGGTGAGCTGCTCGAGTCTGGGGAGTCTGGTACAGCCTGGGGGTCCTGAGACTCT 61
DB 59 AGGTGAGCTGCTGGAGTCTGGGGAGGCGTGGTCAAGCCTGGAGAGTCCCTGAGACTCT 118
QY 62 CCTGTGACCTCTTGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCAAGCTTC 121
DB 119 CCTGTACAGCTGTGATTCACCTTCAGTATGATGCACTGGGTCCGCAAGCTTC 178
QY 122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAATTAATAATATATG 181
DB 179 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGATGGAATTAATAATATATG 238
QY 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCCAGAAACAGCTGTATC 241
DB 239 CAGACTCCGGAAGGGCCGATTCACCATCTCCAGAGCAATTCCAGAAACAGCTGTATC 298
QY 242 TCGAATGAACAGCTGAGAGTGAAGCAACGGCTGTGATTACTGTGCAAAAAAGAA- 300
DB 299 TCGAATGAACAGCTGAGAGTGAAGCAACGGCTGTGATTACTGTGCAAGAGCCGAGC 358
QY 301 -----GGCTACTGGGGCCAGAGAACTCTGTGACCGCTCTCTCAGACCCA 346
DB 359 TCGTGGTTACTTTGACTCTGAGGCGCAGAGAACTCTGTGACCGCTCTCTCAGACCCA 418
QY 347 CCAAGGCTCCGATGTGTCCTCT 371
DB 419 CCAAGGGCCCATCGTCTTCCCT 443

RESULT 10
US-09-472-087-59
Sequence 59, Application US/09472087
Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, EILEEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GITMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-Pf1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 59
LENGTH: 1392
```

```
TYPE: DNA
ORGANISM: Homo sapiens
US-09-472-087-59

Query Match
Best Local Similarity 77.3%; Score 287.4; DB 4; Length 1392;
Matches 334; Conservative 0; Mismatches 36; Indels 15; Gaps 1;

QY 2 AGGTGAGCTGCTCGAGTCTGGGGAGTCTGGTACAGCCTGGGGGTCCTGAGACTCT 61
DB 59 AGGTGAGCTGCTGGAGTCTGGGGAGGCGTGGTCAAGCCTGGAGAGTCCCTGAGACTCT 118
QY 62 CCTGTGACCTCTTGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCAAGCTTC 121
DB 119 CCTGTACAGCTGTGATTCACCTTCAGTATGATGCACTGGGTCCGCAAGCTTC 178
QY 122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAATTAATAATATATG 181
DB 179 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGATGGAATTAATAATATATG 238
QY 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCCAGAAACAGCTGTATC 241
DB 239 CAGACTCCGGAAGGGCCGATTCACCATCTCCAGAGCAATTCCAGAAACAGCTGTATC 298
QY 242 TCGAATGAACAGCTGAGAGTGAAGCAACGGCTGTGATTACTGTGCAAAAAAGAA- 300
DB 299 TCGAATGAACAGCTGAGAGTGAAGCAACGGCTGTGATTACTGTGCAAGAGCCGAGC 358
QY 301 -----GGCTACTGGGGCCAGAGAACTCTGTGACCGCTCTCTCAGACCCA 346
DB 359 TCGTGGTTACTTTGACTCTGAGGCGCAGAGAACTCTGTGACCGCTCTCTCAGACCCA 418
QY 347 CCAAGGCTCCGATGTGTCCTCT 371
DB 419 CCAAGGGCCCATCGTCTTCCCT 443

RESULT 11
US-09-456-090A-101
Sequence 101, Application US/09456090A
Patent No. 6680209
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Valakis, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lomberg, Nils
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERENCE: 020015-000200US
CURRENT APPLICATION NUMBER: US/09/456,090A
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 101
LENGTH: 675
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(675)
OTHER INFORMATION: M2-31H
US-09-456-090A-101

Query Match
Best Local Similarity 77.2%; Score 287.2; DB 4; Length 675;
Matches 332; Conservative 0; Mismatches 38; Indels 12; Gaps 1;

QY 2 AGGTGAGCTGCTCGAGTCTGGGGAGTCTGGTACAGCCTGGGGGTCCTGAGACTCT 61
DB 2 AGGTGAGCTGCTGGAGTCTGGGGAGGCGTGGTCAAGCCTGGAGAGTCCCTGAGACTCT 61
QY 62 CCTGTGACCTCTTGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCAAGCTTC 121
DB 62 CCTGTGACCTCTTGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCAAGCTTC 121
```

QY 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGTAATAATACTATG 181
DB 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGTAATAATACTATG 181
QY 182 CAGACTCCGTAAGGGGCGCATTCATCTCCAGAGCAATTCGAAAGCACTCTGATC 241
DB 182 CAGACTCCGTAAGGGGCGCATTCATCTCCAGAGCAATTCGAAAGCACTCTGATC 241
QY 242 TCGAATGAACAGCTGAGAGCTGAGAGACAGGCTGTGATTAATTAATGTCGGA 294
DB 242 TCGAATGAACAGCTGAGAGCTGAGAGACAGGCTGTGATTAATTAATGTCGGA 301
QY 295 -----AAGAGAGCTACTGCGGCTCAGAGAACTCTGTACCGTCTCTCAGACCCACCA 349
DB 302 TCGGTAATCTTGTGACTGAGGCGCAGAGAACTCTGTGATTAATTAATGTCGGA 361
QY 350 AGGCTCCGATGCTGTCTCCCTCT 371
DB 362 AGGCTCCGATGCTGTCTCCCTCT 383

RESULT 12

US-09-453-234-101
; Sequence 101, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: Genpharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(675)
; OTHER INFORMATION: M2-31H
US-09-453-234-101

Query Match 77.2%; Score 287.2; DB 4; Length 675;

Best Local Similarity 86.9%; Pred. No. 1.8e-84;

Matches 332; Conservative 0; Mismatches 38; Indels 12; Gaps 1;

QY 2 AGGTGACAGCTGCTGAGTCTGGGGGAGTGGGTGACAGCTGGGGGCTCCCTAGACTCT 61
DB 2 AGGTGACAGCTGCTGAGTCTGGGGGAGTGGGTGACAGCTGGGGGCTCCCTAGACTCT 61
QY 62 CCTGTGACGCTCTGATTCACCTTGATGATTATGACATGACCTGGGTCGCGCAGGCTC 121
DB 62 CCTGTGACGCTCTGATTCACCTTGATGATTATGACATGACCTGGGTCGCGCAGGCTC 121
QY 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGTAATAATACTATG 181
DB 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGTAATAATACTATG 181
QY 182 CAGACTCCGTAAGGGGCGCATTCATCTCCAGAGCAATTCGAAAGCACTCTGATC 241
DB 182 CAGACTCCGTAAGGGGCGCATTCATCTCCAGAGCAATTCGAAAGCACTCTGATC 241
QY 242 TCGAATGAACAGCTGAGAGCTGAGAGACAGGCTGTGATTAATTAATGTCGGA 294
DB 242 TCGAATGAACAGCTGAGAGCTGAGAGACAGGCTGTGATTAATTAATGTCGGA 301

DB 242 TCGAATGAACAGCTGAGAGCTGAGAGACAGGCTGTGATTAATTAATGTCGGA 301
QY 295 -----AAGAGAGCTACTGCGGCTCAGAGAACTCTGTACCGTCTCTCAGACCCACCA 349
DB 302 TCGGTAATCTTGTGACTGAGGCGCAGAGAACTCTGTGATTAATTAATGTCGGA 361
QY 350 AGGCTCCGATGCTGTCTCCCTCT 371
DB 362 AGGCTCCGATGCTGTCTCCCTCT 383

RESULT 13

US-09-472-087-28
; Sequence 28, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GITMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 1395
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-472-087-28

Query Match 76.9%; Score 286; DB 4; Length 1395;

Best Local Similarity 86.3%; Pred. No. 6.4e-84;

Matches 335; Conservative 0; Mismatches 35; Indels 18; Gaps 1;

QY 2 AGGTGACAGCTGCTGAGTCTGGGGGAGTGGGTGACAGCTGGGGGCTCCCTAGACTCT 61
DB 59 AGGTGACAGCTGCTGAGTCTGGGGGAGTGGGTGACAGCTGGGGGCTCCCTAGACTCT 118
QY 62 CCTGTGACGCTCTGATTCACCTTGATGATTATGACATGACCTGGGTCGCGCAGGCTC 121
DB 119 CCTGTGACGCTCTGATTCACCTTGATGATTATGACATGACCTGGGTCGCGCAGGCTC 178
QY 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGTAATAATACTATG 181
DB 179 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGTAATAATACTATG 238
QY 182 CAGACTCCGTAAGGGGCGCATTCATCTCCAGAGCAATTCGAAAGCACTCTGATC 241
DB 239 CAGACTCCGTAAGGGGCGCATTCATCTCCAGAGCAATTCGAAAGCACTCTGATC 298
QY 242 TCGAATGAACAGCTGAGAGCTGAGAGACAGGCTGTGATTAATTAATGTCGGA 299
DB 299 TCGAATGAACAGCTGAGAGCTGAGAGACAGGCTGTGATTAATTAATGTCGGA 358
QY 300 -----AGGCTACTGGGCTCAGAGAACTCTGTGATTAATTAATGTCGGA 343
DB 359 GACTGGGCTCTACTTGTGACTGAGGCGCAGAGAACTCTGTGATTAATTAATGTCGGA 418
QY 344 CCACCAAGGCTCCGATGCTCTCTCT 371
DB 419 CCACCAAGGCTCCGATGCTCTCTCTCT 446

RESULT 14

US-09-472-087-57
; Sequence 57, Application US/09472087

```
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 57
; LENGTH: 1395
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-472-087-57

Query Match          76.9%; Score 286; DB 4; Length 1395;
Best Local Similarity 86.3%; Pred. No. 6.4e-84;
Matches 335; Conservative 0; Mismatches 35; Indels 18; Gaps 1;

QY 2 AGGTGACGCTGCTCGAGTCTGGGGAGTGTGCTGTAAGCCTGGGGGCTCCTGAGACTCT 61
DB 59 AGGTGACGCTGCTGAGTCTGGGGAGGCGGTGTGCTGAGCTGGGAGTCCCTGAGACTCT 118
QY 62 CCTGTGACGCTCTGTGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCAAGCTTC 121
DB 119 CCTGTGACGCTCTGTGATTCACCTTCAGTAATGATGCACTGGGTCCGCAAGCTTC 178
QY 122 CAGGCAAGGGGCTGGAGTGGGTGGGAGTATATCATATATGAGAAATTAATACTATG 181
DB 179 CAGGCAAGGGGCTGGAGTGGGTGGGAGTATATGATATGAAATTAATACTATG 238
QY 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAAACAGCTGTATC 241
DB 239 GAGACTCCGTGAAGGGCCGATTCACCATCTCCAGTACAAATTCAGAAACAGCTGTATC 298
QY 242 TGCAAATGAACAGCTGAGAGTGAAGACACGGCTGTGATTACTGTGCGAAAAAGAA-- 299
DB 299 TGCAAATGAACAGCTGAGAGTGAAGACACGGCTGTGATTACTGTGCGAGAGAGAGA 358
QY 300 -----AGGCTACTGGGGCAAGGAAACCTGTGACCGTCTCCTCAGCAC 343
DB 359 GACTGGGGTCTTACTTTGACTTGGGGCCAGGGAAACCTGTGACCGTCTCCTCAGCCT 418
QY 344 CCACCAAGGCTCGGATGTGTCCCTCT 371
DB 419 CCACCAAGGCTCGGATGTGTCCCTCT 446

RESULT 15
US-09-472-087-27
; Sequence 27, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
```

```
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 27
; LENGTH: 1392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-472-087-27

Query Match          76.8%; Score 285.8; DB 4; Length 1392;
Best Local Similarity 86.5%; Pred. No. 7.5e-84;
Matches 333; Conservative 0; Mismatches 37; Indels 15; Gaps 1;

QY 2 AGGTGACGCTGCTCGAGTCTGGGGAGTGTGCTGTAAGCCTGGGGGCTCCTGAGACTCT 61
DB 59 AGGTGACGCTGCTGAGTCTGGGGAGGCGGTGTGCTGAGCTGGGAGTCCCTGAGACTCT 118
QY 62 CCTGTGACGCTCTGTGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCAAGCTTC 121
DB 119 CCTGTGACGCTCTGTGATTCACCTTCAGTAATGATGCACTGGGTCCGCAAGCTTC 178
QY 122 CAGGCAAGGGGCTGGAGTGGGTGGGAGTATATCATATATGAGAAATTAATACTATG 181
DB 179 CAGGCAAGGGGCTGGAGTGGGTGGGAGTATATGATATGAGAAATTAATACTATG 238
QY 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAAACAGCTGTATC 241
DB 239 GAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAAACAGCTGTATC 298
QY 242 TGCAAATGAACAGCTGAGAGTGAAGACACGGCTGTGATTACTGTGCGAAAAAGG--- 298
DB 299 TGCAAATGAACAGCTGAGAGTGAAGACACGGCTGTGATTACTGTGCGAGAGAGTTC 358
QY 299 -----AAGCTACTGGGGCAAGGAAACCTGTGACCGTCTCCTCAGCACCA 346
DB 359 ACTTGGTCTTTTACTTACTTGGGGCAAGGAAACCTGTGACCGTCTCCTCAGCCTCA 418
QY 347 CCACCAAGGCTCGGATGTGTCCCTCT 371
DB 419 CCACCAAGGCTCGGATGTGTCCCTCT 443

Search completed: December 7, 2004, 08:57:55
Job time : 76.8 secs
```


NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 67
LENGTH: 675
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(675)
US-09-453-234-67

Query Match 78.1%; Score 290.4; DB 10; Length 675;
Best Local Similarity 87.4%; Pred. No. 3.3e-86;
Matches 334; Conservative 0; Mismatches 36; Indels 12; Gaps 1;

QY 2 AGGTGAGCTGCTCGAGTCTGGGGGAGTGTGTAAGCTGGGGGCTCCCTGAGACTCT 61
DB 2 AGGTGAGCTGCTCGAGTCTGGGGGAGTGTGTAAGCTGGGGGCTCCCTGAGACTCT 61
QY 62 CCTGTGACGCTCTGTGATTCACCTTTGATGATTATGCACTGGGTCCTCCAGGCTTC 121
DB 62 CCTGTGACGCTCTGTGATTCACCTTTGATGATTATGCACTGGGTCCTCCAGGCTTC 121
QY 122 CAGGCAAGGGGCTGGAGTGGGTGGCACTTATATCATATGTAAGTAATAATACTATG 181
DB 122 CAGGCAAGGGGCTGGAGTGGGTGGCACTTATATGTAAGTAATAATAATACTATG 181
QY 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAAACACGCTGTATC 241
DB 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAAACACGCTGTATC 241
QY 242 TGCATAATGAACAGCTGAGAGCTGAGACACGGCTGTGATTATCTGTGCAAAAAAGG--- 298
DB 242 TGCATAATGAACAGCTGAGAGCTGAGACACGGCTGTGATTATCTGTGCAAAAAAGG--- 298
QY 242 TGCATAATGAACAGCTGAGAGCTGAGACACGGCTGTGATTATCTGTGCAAAAAAGG--- 298
DB 242 TGCATAATGAACAGCTGAGAGCTGAGACACGGCTGTGATTATCTGTGCAAAAAAGG--- 298
QY 299 -----AAGGCTCTGGGGCCAGGAACTGTGTCACCGCTCTCTAGACACCAACA 349
DB 302 TAGGCTACTTTGACTGCTGAGGAGGAGGAACTGTGTCACCGCTCTCTAGACACCAACA 361
QY 350 AAGCTCCGGATGTGTCCCTCT 371
DB 362 AAGGCCCATCGGTCTTCCCTCT 383

RESULT 5
US-10-738-120-9
Sequence 9, Application US/10738120
Publication No. US20040208873A1
GENERAL INFORMATION:
APPLICANT: Teeling, Jessica
APPLICANT: Patren, Paul
APPLICANT: Baadsgaard, Ole
APPLICANT: Hudson, Debra
APPLICANT: Petersen, Jorgen
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST INTERLEUKIN 8 (IL-8)
FILE REFERENCE: MX1-278
CURRENT APPLICATION NUMBER: US/10/738,120
CURRENT FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: 60/433,728
PRIOR FILING DATE: 2002-12-16
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 342
TYPE: DNA
ORGANISM: Homo sapiens
US-10-738-120-9

Query Match 78.0%; Score 290.2; DB 18; Length 342;
Best Local Similarity 92.7%; Pred. No. 3e-86;
Matches 316; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

QY 2 AGGTGAGCTGCTCGAGTCTGGGGGAGTGTGTAAGCTGGGGGCTCCCTGAGACTCT 61
DB 2 AGGTGAGCTGCTCGAGTCTGGGGGAGTGTGTAAGCTGGGGGCTCCCTGAGACTCT 61
QY 62 CCTGTGACGCTCTGTGATTCACCTTTGATGATTATGCACTGGGTCCTCCAGGCTTC 121
DB 62 CCTGTGACGCTCTGTGATTCACCTTTGATGATTATGCACTGGGTCCTCCAGGCTTC 121
QY 122 CAGGCAAGGGGCTGGAGTGGGTGGCACTTATATCATATGTAAGTAATAATACTATG 181
DB 122 CAGGCAAGGGGCTGGAGTGGGTGGCACTTATATCATATGTAAGTAATAATACTATG 181
QY 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAAACACGCTGTATC 241
DB 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAAACACGCTGTATC 241
QY 242 TGCATAATGAACAGCTGAGAGCTGAGACACGGCTGTGATTATCTGTGCAAAAAAGG 299
DB 242 TGCATAATGAACAGCTGAGAGCTGAGACACGGCTGTGATTATCTGTGCAAAAAAGG 299
QY 300 AAGCTACTGGGGCCAGGAACTGTGTCACCGTCTCTCAG 340
DB 302 TAGCTACTGGGGCCAGGAACTGTGTCACCGTCTCTCAG 342

RESULT 6
US-09-453-234-59
Sequence 59, Application US/09453234
Publication No. US2003009195A1
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Walkier, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lomborg, Nils
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: Genpharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 59
LENGTH: 675
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: M1-5H
NAME/KEY: CDS
LOCATION: (1)..(675)
US-09-453-234-59

Query Match 77.6%; Score 288.8; DB 10; Length 675;
Best Local Similarity 87.2%; Pred. No. 1.1e-85;
Matches 333; Conservative 0; Mismatches 37; Indels 12; Gaps 1;

QY 2 AGGTGAGCTGCTCGAGTCTGGGGGAGTGTGTAAGCTGGGGGCTCCCTGAGACTCT 61
DB 2 AGGTGAGCTGCTCGAGTCTGGGGGAGTGTGTAAGCTGGGGGCTCCCTGAGACTCT 61
QY 62 CCTGTGACGCTCTGTGATTCACCTTTGATGATTATGCACTGGGTCCTCCAGGCTTC 121
DB 62 CCTGTGACGCTCTGTGATTCACCTTTGATGATTATGCACTGGGTCCTCCAGGCTTC 121
QY 122 CAGGCAAGGGGCTGGAGTGGGTGGCACTTATATCATATGTAAGTAATAATACTATG 181
DB 122 CAGGCAAGGGGCTGGAGTGGGTGGCACTTATATCATATGTAAGTAATAATACTATG 181
QY 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAAACACGCTGTATC 241
DB 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAAACACGCTGTATC 241

QY 242 TGCATATGAACAGCTGAGAGTGAAGACACGGCTGTGATTAATCTGTGCGAAAAGG--- 298
| | | | |
Db 242 TGCATATGAACAGCTGAGAGTGAAGACACGGCTGTGATTAATCTGTGCGAAAAGG 301
QY 299 -----AAGCTACTGGGGCCAGGGAACCTGTGACCGCTCTCTGAGCAGCCAGCA 349
| | | | |
Db 302 TCGGGTACTTTGACTTATGGGGCCAGGGAACCTGTGACCGCTCTCTGAGCAGCCAGCA 361
QY 350 AGGCTCCGGATGTGTTCCCTCT 371
| | | | |
Db 362 AGGGCCCATCGGTCTTCCCTCT 383
| | | | |

RESULT 7
US-09-453-234-91
; Sequence 91, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(675)
; OTHER INFORMATION: M2-11H
US-09-453-234-91

Query Match 77.6%; Score 288.8; DB 10; Length 675;
Best Local Similarity 87.2%; Pred. No. 1.1e-85;
Matches 333; Conservative 0; Mismatches 37; Indels 12; Gaps 1;

QY 2 AGGTGAGCTGCTCGAGTCTGGGGAGTGTGGTACAGCTTGGGGGTCCTGAGACTCT 61
| | | | |
Db 2 AGGTGAGCTGCTGGAGTCTGGGGAGGCGTGTGTCCAGCTGGAGGTCCCTGAGACTCT 61
QY 62 CCGTGACAGCTCTGATTCACCTTGAAGATTATGATTCAGCTGGGGTCCCGCAGGCTC 121
| | | | |
Db 62 CCGTGACAGCTCTGATTCACCTTGAAGATTATGATTCAGCTGGGGTCCCGCAGGCTC 121
QY 122 CAGGCAAGGGGCTGAGTGGTGGGCACTATATATGATGAGAGTAATAATATCTATG 181
| | | | |
Db 122 CAGGCAAGGGGCTGAGTGGTGGGCACTATATATGATGAGAGTAATAATATCTATG 181
QY 122 CAGGCAAGGGGCTGAGTGGTGGGCACTATATATGATGAGAGTAATAATATCTATG 181
| | | | |
Db 122 CAGGCAAGGGGCTGAGTGGTGGGCACTATATATGATGAGAGTAATAATATCTATG 181
QY 162 CAGACTCCGTGAAGGGCCGATTCACCATCTCAGAGACAATTCAGAAACAAGCTGTATC 241
| | | | |
Db 162 CAGACTCCGTGAAGGGCCGATTCACCATCTCAGAGACAATTCAGAAACAAGCTGTATC 241
QY 242 TGCATATGAACAGCTGAGAGTGAAGACACGGCTGTGATTAATCTGTGCGAAAAGG--- 298
| | | | |
Db 242 TGCATATGAACAGCTGAGAGTGAAGACACGGCTGTGATTAATCTGTGCGAAAAGG 301
QY 299 -----AAGCTACTGGGGCCAGGGAACCTGTGACCGCTCTCTGAGCAGCCAGCA 349
| | | | |
Db 302 TCGGGTACTTTGACTTATGGGGCCAGGGAACCTGTGACCGCTCTCTGAGCAGCCAGCA 361
QY 350 AGGCTCCGGATGTGTTCCCTCT 371
| | | | |
Db 362 AGGGCCCATCGGTCTTCCCTCT 383
| | | | |

Db 362 AGGGCCCATCGGTCTTCCCTCT 383
| | | | |

RESULT 8
US-09-453-234-55

; Sequence 55, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 677
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: M1-3H
; NAME/KEY: CDS
; LOCATION: (3)..(677)
US-09-453-234-55

Query Match 77.5%; Score 288.2; DB 10; Length 677;
Best Local Similarity 86.9%; Pred. No. 1.8e-85;
Matches 333; Conservative 0; Mismatches 38; Indels 12; Gaps 1;

QY 1 GAGTGCAGCTGCTCGAGTCTGGGGAGTGTGGTACAGCTTGGGGGTCCTGAGACTC 60
| | | | |
Db 3 GAGTGCAGCTGCTCGAGTCTGGGGAGGCGTGTGTCCAGCTGGAGGTCCCTGAGACTC 62
QY 61 TCGTGACAGCTCTGATTCACCTTGAAGATTATGATTCAGCTGGGGTCCCGCAGGCT 120
| | | | |
Db 63 TCGTGACAGCTCTGATTCACCTTGAAGATTATGATTCAGCTGGGGTCCCGCAGGCT 122
QY 121 CAGGCAAGGGGCTGAGTGGTGGGCACTATATATGATGAGAGTAATAATATCTAT 180
| | | | |
Db 123 CAGGCAAGGGGCTGAGTGGTGGGCACTATATATGATGAGAGTAATAATATCTAT 182
QY 181 GCAAGCTCCGTGAAGGGCCGATTCACCATCTCAGAGACAATTCAGAAACAAGCTGTAT 240
| | | | |
Db 183 GCAAGCTCCGTGAAGGGCCGATTCACCATCTCAGAGACAATTCAGAAACAAGCTGTAT 242
QY 241 CTGCATATGAACAGCTGAGAGTGAAGACACGGCTGTGATTAATCTGTGCGAAAAGG-- 298
| | | | |
Db 243 CTGCATATGAACAGCTGAGAGTGAAGACACGGCTGTGATTAATCTGTGCGAAAAGG 302
QY 299 -----AAGCTACTGGGGCCAGGGAACCTGTGACCGCTCTCTGAGCAGCCAGCA 348
| | | | |
Db 303 ATCGGGTACTTTGACTTATGGGGCCAGGGAACCTGTGACCGCTCTCTGAGCAGCCAGCA 362
QY 349 AAGGCTCCGGATGTGTTCCCTCT 371
| | | | |
Db 363 AAGGGCCCATCGGTCTTCCCTCT 385
| | | | |

RESULT 9
US-10-292-088-37

; Sequence 37, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE

```

; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 37
; LENGTH: 1398
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-292-088-37

Query Match      77.4%; Score 287.8; DB 15; Length 1398;
Best Local Similarity 86.4%; Pred. No. 3,1e-85;
Matches 338; Conservative 0; Mismatches 32; Indels 21; Gaps 1;

QY 2 AGGTGAGCTGCTCGAGTCTGGGGAGTCTGTGTACAGCTTGGGGGCTCTTGAGACTCT 61
DB 59 AGGTGAGCTGTGTGAGTCTGGGGAGGCGTGTGTCAGCTGGAGGTCCTTGAGACTCT 118
QY 62 CCTGTGACAGCTCTGTGATTCACCTTTGATGATTATGCACTGGGTCCTGCAAGCTTC 121
DB 119 CCGTGACAGCTCTGTGATTCACCTTGATGATTATGCACTGGGTCCTGCAAGCTTC 178
QY 122 CAGGCAAGGGGCTGAGTGGGTGGAGTATATCATATGAGTAAGTAATAATACTATG 181
DB 179 CAGGCAAGGGGCTGAGTGGGTGGAGTATATGATATGTAAGTAATAATACTATG 238
QY 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAAACGCTGTATC 241
DB 239 CAACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAAACGCTGTATC 298
QY 242 TGCATATGAACAGCTGAGAGTGAAGACACGGCTGTATTACTGTGGAAAAAGAAAG 301
DB 299 TGCATATGAACAGCTGAGAGTGAAGACACGGCTGTATTACTGTGGAAAAAGAAAG 358
QY 302 G-----CTACTGGGGCCAGGAAACCTGTGACCGTCTCTCAG 340
DB 359 GTAAAGAGTGTCTGTGCTGTGACTACTGGGGCCAGGAAATCTGTGACCGTCTCTCAG 418
QY 341 CACCCACCAAGGCTCCGATGTGTCTCTCT 371
DB 419 CCTCCACCAAGGGCCCATCGGTCTTCCCT 449

RESULT 10
US-10-153-382-12
; Sequence 12, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PRIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
; LENGTH: 1392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-153-382-12

Query Match      77.3%; Score 287.4; DB 14; Length 1392;
Best Local Similarity 86.8%; Pred. No. 4.2e-85;
Matches 334; Conservative 0; Mismatches 36; Indels 15; Gaps 1;

```

```

QY 2 AGGTGAGCTGCTCGAGTCTGGGGAGTCTGTGTACAGCTTGGGGGCTCTTGAGACTCT 61
DB 59 AGGTGAGCTGTGTGAGTCTGGGGAGGCGTGTGTCAGCTGGAGGTCCTTGAGACTCT 118
QY 62 CCTGTGACAGCTCTGTGATTCACCTTTGATGATTATGCACTGGGTCCTGCAAGCTTC 121
DB 119 CCGTGACAGCTCTGTGATTCACCTTGATGATTATGCACTGGGTCCTGCAAGCTTC 178
QY 122 CAGGCAAGGGGCTGAGTGGGTGGAGTATATCATATGAGTAAGTAATAATACTATG 181
DB 179 CAGGCAAGGGGCTGAGTGGGTGGAGTATATGATATGTAAGTAATAATACTATG 238
QY 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAAACGCTGTATC 241
DB 239 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAAACGCTGTATC 298
QY 242 TGCATATGAACAGCTGAGAGTGAAGACACGGCTGTATTACTGTGGAAAAAGAA- 300
DB 299 TGCATATGAACAGCTGAGAGTGAAGACACGGCTGTATTACTGTGGAAAAAGAA- 358
QY 301 -----GCTACTGGGGCCAGGAAACCTGTGACCGTCTCTCAGACCA 346
DB 359 TCGTGATTACTTTGACTACTGGGGCCAGGAAACCTGTGACCGTCTCTCAGACCA 418
QY 347 CCAAGGCTCCGATGTGTCTCTCT 371
DB 419 CCAAGGGCCCATGTGTCTTCCCT 443

RESULT 11
US-10-612-497-30
; Sequence 30, Application US/10612497
; Publication No. US20040228858A1
; GENERAL INFORMATION:
; APPLICANT: Douglas C. Hanson
; APPLICANT: Mark J. Neveu
; APPLICANT: Eileen E. Mueller
; APPLICANT: Jeffrey H. Hanke
; APPLICANT: Steven C. Gilman
; APPLICANT: C. Geoffrey Davis
; APPLICANT: Jose R. Corvalan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1 DIV1
; CURRENT APPLICATION NUMBER: US/10/612,497
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 09/472087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 30
; LENGTH: 1392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-612-497-30

Query Match      77.3%; Score 287.4; DB 18; Length 1392;
Best Local Similarity 86.8%; Pred. No. 4.2e-85;
Matches 334; Conservative 0; Mismatches 36; Indels 15; Gaps 1;

```

```
QY 182 CAGACTCCGTGAAGGCGCATTCACCATCTCCAGAGACAATTCAGAAACACGCTGTATC 241
| | | | |
Db 239 CAGACTCCGCGAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAAACACGCTGTATC 298
QY 242 TGCATAATGAACAGCTGAGAGAGAGACCGCTGTATTAATCTGTGCGAAAAAGAA- 300
| | | | |
Db 299 TGCATAATGAACAGCTGAGAGAGAGACCGCTGTATTAATCTGTGCGAAAAAGAA- 358
QY 301 -----GCTACTGAGGCGCAGAGAACCTGTGTACCGTCTCTCAGACCCCA 346
| | | | |
Db 359 TCGTGGGTACTTGTACTGTGGGGCCAGGGAACCTGTGTACCGTCTCTCAGACCCCA 418
QY 347 CCAAGGCTCCGATGTGTTCCCTCT 371
| | | | |
Db 419 CCAAGGCGCCATCGGTCTTCCCTCT 443
```

RESULT 12

```
US-10-612-497-59
; Sequence 59, Application US/10612497
; Publication No. US20040228858A1
; GENERAL INFORMATION:
; APPLICANT: Douglas C. Hanson
; APPLICANT: Mark J. Neveu
; APPLICANT: Eileen E. Mueller
; APPLICANT: Jeffrey H. Hanke
; APPLICANT: Steven C. Gilman
; APPLICANT: C. Geoffrey Davis
; APPLICANT: Jose R. Corvalan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-Pf1 DIV1
; CURRENT APPLICATION NUMBER: US/10/612,497
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 09/472087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 59
; LENGTH: 1392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-612-497-59
```

Query Match 77.3%; Score 287.4; DB 18; Length 1392;
Best Local Similarity 86.8%; Pred. No. 4.2e-85;
Matches 334; Conservative 0; Mismatches 36; Indels 15; Gaps 1;

```
QY 2 AGGTGACAGCTGCTCGAGTCTGGGGAGTGTGTGTAACAGCTGGGGGATCCCTGAGACTCT 61
| | | | |
Db 59 AGGTGACAGCTGCTGAGTCTGGGGAGGCGTGTGTAACAGCTGGGGGATCCCTGAGACTCT 118
QY 62 CCTGTGACAGCTCTGATTCACCTTTGATGATTAATGCACTGAGTCCGCGAGGCTC 121
| | | | |
Db 119 CCTGTGACAGCTCTGATTCACCTTTGATGATTAATGCACTGAGTCCGCGAGGCTC 178
QY 122 CAGGCAAGGGGCTGAGTGGGTGCGAGTTATATATATGAGAACTAATAATTAATG 181
| | | | |
Db 179 CAGGCAAGGGGCTGAGTGGGTGCGAGTTATATATATGAGAACTAATAATTAATG 238
QY 182 CAGACTCCGTGAAGGCGCATTCACCATCTCCAGAGACAATTCAGAAACACGCTGTATC 241
| | | | |
Db 239 CAGACTCCGCGAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAAACACGCTGTATC 298
QY 242 TGCATAATGAACAGCTGAGAGAGAGACCGCTGTATTAATCTGTGCGAAAAAGAA- 300
| | | | |
Db 299 TGCATAATGAACAGCTGAGAGAGAGACCGCTGTATTAATCTGTGCGAAAAAGAA- 358
QY 301 -----GGCTACTGGGGCCAGGGAACCTGTGTACCGTCTCTCAGACCCCA 346
| | | | |
Db 359 TCGTGGGTACTTGTACTGTGGGGCCAGGGAACCTGTGTACCGTCTCTCAGACCCCA 418
```

```
QY 347 CCAAGGCTCCGATGTGTTCCCTCT 371
| | | | |
Db 419 CCAAGGCGCCATCGGTCTTCCCTCT 443
```

RESULT 13

```
US-10-776-649-30
; Sequence 30, Application US/10776649
; Publication No. US20040228861A1
; GENERAL INFORMATION:
; APPLICANT: Douglas C. Hanson
; APPLICANT: Mark J. Neveu
; APPLICANT: Eileen E. Mueller
; APPLICANT: Jeffrey H. Hanke
; APPLICANT: Steven C. Gilman
; APPLICANT: C. Geoffrey Davis
; APPLICANT: Jose R. Corvalan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-Pf1 DIV2
; CURRENT APPLICATION NUMBER: US/10/776,649
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 10/612497
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 09/472087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 30
; LENGTH: 1392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-776-649-30
```

Query Match 77.3%; Score 287.4; DB 18; Length 1392;
Best Local Similarity 86.8%; Pred. No. 4.2e-85;
Matches 334; Conservative 0; Mismatches 36; Indels 15; Gaps 1;

```
QY 2 AGGTGACAGCTGCTCGAGTCTGGGGAGTGTGTGTAACAGCTGGGGGATCCCTGAGACTCT 61
| | | | |
Db 59 AGGTGACAGCTGCTGAGTCTGGGGAGGCGTGTGTAACAGCTGGGGGATCCCTGAGACTCT 118
QY 62 CCTGTGACAGCTCTGATTCACCTTTGATGATTAATGCACTGAGTCCGCGAGGCTC 121
| | | | |
Db 119 CCTGTGACAGCTCTGATTCACCTTTGATGATTAATGCACTGAGTCCGCGAGGCTC 178
QY 122 CAGGCAAGGGGCTGAGTGGGTGCGAGTTATATATATGAGAACTAATAATTAATG 181
| | | | |
Db 179 CAGGCAAGGGGCTGAGTGGGTGCGAGTTATATATATGAGAACTAATAATTAATG 238
QY 182 CAGACTCCGTGAAGGCGCATTCACCATCTCCAGAGACAATTCAGAAACACGCTGTATC 241
| | | | |
Db 239 CAGACTCCGCGAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAAACACGCTGTATC 298
QY 242 TGCATAATGAACAGCTGAGAGAGAGACCGCTGTATTAATCTGTGCGAAAAAGAA- 300
| | | | |
Db 299 TGCATAATGAACAGCTGAGAGAGAGACCGCTGTATTAATCTGTGCGAAAAAGAA- 358
QY 301 -----GCTACTGAGGCGCAGAGAACCTGTGTACCGTCTCTCAGACCCCA 346
| | | | |
Db 359 TCGTGGGTACTTGTACTGTGGGGCCAGGGAACCTGTGTACCGTCTCTCAGACCCCA 418
QY 347 CCAAGGCTCCGATGTGTTCCCTCT 371
| | | | |
Db 419 CCAAGGCGCCATCGGTCTTCCCTCT 443
```

RESULT 14

```
US-10-776-649-59
; Sequence 59, Application US/10776649
; Publication No. US20040228861A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Douglas C. Hanson
; APPLICANT: Mark J. Neveu
; APPLICANT: Eileen E. Mueller
; APPLICANT: Jeffrey H. Hanke
; APPLICANT: Steven C. Gilman
; APPLICANT: C. Geoffrey Davis
; APPLICANT: Jose R. Corvalan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-Pf1 DIV2
; CURRENT APPLICATION NUMBER: US/10/776,649
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 10/612497
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 09/472087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 1392
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-776-649-59.

Query Match      77.3%; Score 287.4; DB 18; Length 1392;
Best Local Similarity 86.8%; Pred. No. 4,2e-85;
Matches 334; Conservative 0; Mismatches 36; Indels 15; Gaps 1;

QY 2 AGGTGACGCTGCTCGAGTCTGGGGGAGTGTGTACAGCTGGGGGTCCTGAGACTCT 61
DB 59 AGGTGACGCTGCTGGAGTCTGGGGGAGGCGTGTGTCAGGCTGGAGGTCCTGAGACTCT 118
QY 62 CCTGTGACAGCTCTGTGATTCACCTTTGATGATTAATCCATGCACTGGGTCCGCGAGCTC 121
DB 119 CCGTGTACAGCGTCTGATTCACCTTCAGTATGATGCACTGGGTCCGCGAGCTC 178
QY 122 CAGGCAAGGGGCTGAGTGGTGGCGAGTTATATCATATGATGAGTAATAATTAATCTATG 181
DB 179 CAGGCAAGGGGCTGAGTGGTGGCGAGTTATATGATGAGTAATAATAAACAATTAATG 238
QY 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAGACAAGCTGTATC 241
DB 239 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAGACAAGCTGTATC 298
QY 242 TGCATATGAACAGCTGAGAGCTGAGAGACACGGCTGTGTATTACTGTGGAAAAAGAA- 300
DB 299 TGCATATGAACAGCTGAGAGCTGAGAGACACGGCTGTGTATTACTGTGGAGAGCGGAGC 358
QY 301 -----GGCTACTGGGGGCCAGAGAACTCTGTCAACCGTCTCTCTAGCACCA 346
DB 359 TGCCTGGTTACTTTGACTACTGGGGCCAGAGAACTCTGTCAACCGTCTCTCTAGCACCA 418
QY 347 CCAAGGCTCCGAGATGTGTCCTCT 371
DB 419 CCAAGGCCCCATGGGTCTTCCCT 443

```

```

RESULT 15
US-09-453-234-101
; Sequence 101, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: Genpharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01

```

```

; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(675)
; OTHER INFORMATION: M2-31H
; US-09-453-234-101

Query Match      77.2%; Score 287.2; DB 10; Length 675;
Best Local Similarity 86.9%; Pred. No. 3,8e-85;
Matches 332; Conservative 0; Mismatches 38; Indels 12; Gaps 1;

QY 2 AGGTGACGCTGCTCGAGTCTGGGGGAGTGTGTACAGCTGGGGGTCCTGAGACTCT 61
DB 2 AGGTGACGCTGCTGGAGTCTGGGGGAGGCGTGTGTCAGGCTGGAGGTCCTGAGACTCT 61
QY 62 CCTGTGACAGCTCTGTGATTCACCTTTGATGATTAATCCATGCACTGGGTCCGCGAGCTC 121
DB 62 CCTGTGACAGCTCTGTGATTCACCTTCAGTATGATGCACTGGGTCCGCGAGCTC 121
QY 122 CAGGCAAGGGGCTGAGTGGTGGCGAGTTATATCATATGATGAGTAATAATTAATCTATG 181
DB 122 CAGGCAAGGGGCTGAGTGGTGGCGAGTTATATCATATGATGAGTAATAATAATTAATG 181
QY 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAGACAAGCTGTATC 241
DB 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAGACAAGCTGTATC 241
QY 242 TGCATATGAACAGCTGAGAGCTGAGAGACACGGCTGTGTATTACTGTGGAAAA----- 294
DB 242 TGCATATGAACAGCTGAGAGCTGAGAGACACGGCTGTGTATTACTGTGGAGACTGGA 301
QY 295 -----AAGGAAGCTACTGAGGCGCAGAGAACTCTGTCAACCGTCTCTAGCACCA 349
DB 302 TCGGTAATTTGACTACTGGGGCCAGAGAACTCTGTCAACCGTCTCTAGCCTCACCA 361
QY 350 AGGCTCCGAGATGTGTCCTCT 371
DB 362 AGGCCCCATGGGTCTTCCCT 383

```

Search completed: December 7, 2004, 14:26:31
Job time : 320.733 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 06:11:35 : Search time 2170.93 Seconds
(without alignments)
6244.126 Million cell updates/sec

Title: US-09-403-107-145

Perfect score: 372
Sequence: 1 gaggcgagcgagcgagcgagc.....ctccgagatggtccctcta 372

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss81:*
9: gb_gss82:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	283.2	76.1	503	2	AM402572 UI-HF-BKO
2	279.4	75.1	648	4	BG340670 602462250
3	278	74.7	918	5	BQ710537 AGENCOURT
4	277.8	74.7	950	5	BQ708952 AGENCOURT
5	277	74.5	621	6	CD687626 EST1417 h
6	276.8	74.4	907	4	BQ708724 AGENCOURT
7	276.8	74.4	1001	4	BM914366 AGENCOURT
8	274.2	73.7	678	4	BG340648 602462226
9	274.2	73.7	788	4	BG342203 602462979
10	274.2	73.7	870	4	BG759649 602713342
11	274.2	73.7	964	4	BF663281 602144406
12	274.2	73.7	991	2	BF974524 602243430
13	274.2	73.7	1010	2	BF663436 602144593
14	273.2	73.4	846	4	BG755572 602716255
15	272.6	73.3	912	4	BG756211 602713521
16	272.6	73.3	930	4	BG755605 602716292
17	271.8	73.1	413	5	BX344075 BX344075
18	270.6	72.7	516	2	AM401728 UI-HF-BKO
19	270	72.6	761	4	BG757080 602715111
20	269.8	72.5	937	5	BQ706852 AGENCOURT
21	269.6	72.4	436	2	AM402311 UI-HF-BKO
22	269.4	72.4	663	4	BG686759 602650729
23	268.8	72.3	962	5	BQ706534 AGENCOURT
24	268.8	72.3	962	5	BQ706534 AGENCOURT

25	268.8	72.3	1000	5	BQ712690 AGENCOURT
26	268.2	72.1	999	5	BQ707443 AGENCOURT
27	267	71.8	891	5	BQ709554 AGENCOURT
28	267	71.8	886	5	BQ710656 AGENCOURT
29	266.8	71.7	894	5	BQ708235 AGENCOURT
30	266.6	71.7	456	4	BG503730 602549705
31	266.6	71.7	902	5	BX436850 BX436850
32	266.4	71.6	1328	4	BM920476 AGENCOURT
33	265.8	71.5	413	5	BX399298 AGENCOURT
34	264.6	71.1	958	5	BQ709987 AGENCOURT
35	263.8	70.9	896	5	BQ717993 AGENCOURT
36	263.2	70.8	750	2	BF976111 602244955
37	262.4	70.5	430	5	BX480277 DFFZP6860
38	262.4	70.5	906	5	BU151579 AGENCOURT
39	262.2	70.5	889	5	BQ709105 AGENCOURT
40	262.2	70.5	925	5	BQ706858 AGENCOURT
41	261.4	70.3	536	2	AM402624 UI-HF-BKO
42	259.8	69.8	891	5	BU150876 AGENCOURT
43	259.8	69.8	1007	4	BM914489 AGENCOURT
44	258.6	69.5	802	4	BG756245 602713557
45	258	69.4	870	5	BQ711138 AGENCOURT

ALIGNMENTS

RESULT 1
AM402572 503 bp mRNA linear EST 16-FEB-2000
LOCUS UI-HF-BKO-ax-b-12-0-UI.r1 NIH-MGC_36 Homo sapiens cDNA clone
DEFINITION IMAGE:3055079 5', mRNA sequence.
ACCESSION AM402572
VERSION AM402572.1 GI:6921271
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
Location/Qualifiers

FEATURES
source 1..503

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3055079"
/cistype="lymph"
/cistype="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="PHIOB (UT1)"
/note="Vector: pTZ19-Pac; Site 1: NotI; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb) directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 76.1%; Score 283.2; DB 2; Length 503;
Best Local Similarity 85.5%; Pred. No. 4,4e-73;

Matches 337; Conservative 0; Mismatches 33; Indels 24; Gaps 1;

QY 2 AGGTGAGCTGCTCGAGTCTGGGGAGTGTGTGTAACCTGGGGGTCTCTGAGACTCT 61
 |||||
 DB 44 AGGTGAGCTGCTGAGTCTGGGGAGTGTGTGTAACCTGGGGGTCTCTGAGACTCT 103
 |||||
 QY 62 CCGTGTGAGCTGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 121
 |||||
 DB 104 CCGTGTGAGCTGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 163
 |||||
 QY 122 CAGGCAAGGGGCTGAGTGTGGGAGTGTATATCATATGATGAGAAATTAATTAAT 181
 |||||
 DB 164 CAGGCAAGGGGCTGAGTGTGGGAGTGTATATCATATGATGAGAAATTAATTAAT 223
 |||||
 QY 182 CAGACTCCGTGAAAGGGCCGATTCACATCTCCAGAGCAATTCAGAAACAGCTGTATC 241
 |||||
 DB 224 CAGACTCCGTGAAAGGGCCGATTCACATCTCCAGAGCAATTCAGAAACAGCTGTATC 283
 |||||
 QY 242 TCGCAATGAAACAGCTGAGAGTGAAGACAGGCTGTATTACTGTGCGAAAA----- 295
 |||||
 DB 284 TCGCAATGAAACAGCTGAGAGTGAAGACAGGCTGTATTACTGTGCGAAAA----- 343
 |||||
 QY 296 -----AGGAAGGCTACTGAGGCGGAGGAAACCTGTGACCGTCTCT 337
 |||||
 DB 344 ATTACGATTTTGAAGTGCACAAACTAGGGGCGAGGGAACCTGTGACCGTCTCT 403
 |||||
 QY 338 CAGCAACCCCAAGGCTCGGATGTGTCTCTCT 371
 |||||
 DB 404 CAGCTTCCACCAAGGGCCATCGGTCTTCCCTCT 437
 |||||

RESULT 2
 BG340670 648 bp mRNA linear EST 27-FEB-2001
 LOCUS BG340670
 DEFINITION 602462250F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4574941 5',
 mRNA sequence.
 ACCESSION BG340670
 VERSION BG340670.1 GI:13147108
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 1 (bases 1 to 648)
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Louis M. Straub, M.D., Ph.D.
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 Plate: LNCM1285 row: d column: 14
 High quality sequence stop: 648.
 Location/Qualifiers
 1..648
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4574941"
 /tissue_type="Primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH_MGC_48"
 /note="Organ: B-cells; Vector: pMT7; Site: 1: XhoI;
 Site: 2: EcoRI; CDNA made by oligo-dT priming;
 directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAAGG(9). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH-MGC Library."

Query Match 75.1%; Score 279.4; DB 4; Length 648;
 Best Local Similarity 86.3%; Pred. No. 6.3e-72;
 Matches 322; Conservative 0; Mismatches 46; Indels 5; Gaps 1;

ORIGIN

QY 1 GAGGTGAGCTGCTGAGTCTGGGGAGTGTGTGTAACCTGGGGGTCTCTGAGACTC 60
 |||||
 DB 82 GAGGTGAGCTGCTGAGTCTGGGGAGTGTGTGTAACCTGGGGGTCTCTGAGACTC 141
 |||||
 QY 61 TCGTGTGAGCTGCTGAGTCTGGGGAGTGTGTGTAACCTGGGGGTCTCTGAGACTC 120
 |||||
 DB 142 TCGTGTGAGCTGCTGAGTCTGGGGAGTGTGTGTAACCTGGGGGTCTCTGAGACTC 201
 |||||
 QY 121 CAGGCAAGGGGCTGAGTGTGGGAGTGTATATCATATGATGAGAAATTAATTAAT 180
 |||||
 DB 202 CAGGCAAGGGGCTGAGTGTGGGAGTGTATATCATATGATGAGAAATTAATTAAT 261
 |||||
 QY 181 GCAAGTCCGTGAAAGGGCCGATTCACATCTCCAGAGCAATTCAGAAACAGCTGTAT 240
 |||||
 DB 262 GCAAGTCCGTGAAAGGGCCGATTCACATCTCCAGAGCAATTCAGAAACAGCTGTAT 321
 |||||
 QY 241 CTGCAATGAAACAGCTGAGAGTGAAGACAGGCTGTATTACTGTGCGAAAA----- 296
 |||||
 DB 322 CTGCAATGAAACAGCTGAGAGTGAAGACAGGCTGTATTACTGTGCGAAAA----- 381
 |||||
 QY 297 -GGAAGGCTACTGAGGGCCAGGAAACCTGTGACCGTCTCTCAGACCCCAAGGCTC 355
 |||||
 DB 382 GTGATGCTGAGTGTGGGCGAGGAAACCTGTGACCGTCTCTCAGACCCCAAGGCTC 441
 |||||
 QY 356 CGGATGTGTTCC 368
 |||||
 DB 442 CGGATGTGTTCC 454
 |||||

RESULT 3
 BQ710537 918 bp mRNA linear EST 16-JUL-2002
 LOCUS BQ710537
 DEFINITION AGENCOURT 8354676 NIH_MGC_113 Homo sapiens CDNA clone IMAGE:6281052
 5', mRNA sequence.
 ACCESSION BQ710537
 VERSION BQ710537.1 GI:21849436
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 1 (bases 1 to 918)
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 Plate: LNCM2473 row: d column: 13
 High quality sequence stop: 612.
 Location/Qualifiers
 1..918
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6281052"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH_MGC_113"

/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 74.7%; Score 278; DB 5; Length 918;
Best Local Similarity 85.1%; Pred. No. 1.8e-71;
Matches 330; Conservative 0; Mismatches 40; Indels 18; Gaps 1;

QY 2 AGGTGAGCTGCTCTGAGTCTGGGGAGTCTGTGTAACAGCTGGGGGTCCTGAGACTCT 61
DB 126 AGGTGAGCTGCTGAGTCTGGGGAGTCTGTGTAACAGCTGGGGGTCCTGAGACTCT 185
QY 62 CCTGTGACGCTCTGATTCACCTTTGATGATTAATGCACTGGTCCGACAGCTC 121
DB 186 CCTGTGACGCTCTGATTCACCTTTGATGATTAATGCACTGGTCCGACAGCTC 245
QY 122 CAGGCAAGGGGCTGAGTGGTGGCAGTTATATCATATGATGGAATTAATACTATG 181
DB 246 CAGGCAAGGGGCTGAGTGGTGGCAGTTATATCATATGATGGAATTAATACTATG 305
QY 182 CAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGCAATTCGAAGAACGCTGTATC 241
DB 306 CAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGCAATTCGAAGAACGCTGTATC 365
QY 242 TGCATATGAACAGCTGAGAGTGAAGACACGGCTGTATTACTGTGGGAAAGAA- 300
DB 366 TGCATATGAACAGCTGAGAGTGAAGACACGGCTGTATTACTGTGGGAAAGAA- 425
QY 301 -----GGCTACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCTCAGCAC 343
DB 426 TGGTATGATGTTTATGATGAGTCTGGGGGCAAGGAGCAACGTCACCGTCTCTCAGCCT 485
QY 344 CCAACCAAGGCTCCGATGTGTTCCCTCT 371
DB 486 CCAACCAAGGCTCCGATGTGTTCCCTCT 513

RESULT 4
BQ708952 950 bp mRNA linear EST 16-JUL-2002
LOCUS AGENCOURT 8485030 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301022
DEFINITION 5', mRNA Sequence.
ACCESSION BQ708952
VERSION BQ708952.1 GI:21847851
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 950)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.jnl.gov
plate: LNCM2516 row: d column: 15
High quality sequence stop: 694.
Location/Qualifiers
1. .950
/organism="Homo sapiens"

FEATURES

source

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6301022"
/lab_host="DH10B (phage-resistant)"
/clone_1b="NIH MGC 113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 74.7%; Score 277.8; DB 5; Length 950;
Best Local Similarity 85.2%; Pred. No. 2e-71;
Matches 328; Conservative 0; Mismatches 42; Indels 15; Gaps 1;

QY 2 AGGTGAGCTGCTCTGAGTCTGGGGAGTCTGTGTAACAGCTGGGGGTCCTGAGACTCT 61
DB 127 AGGTGAGTGTGAGTCTGGGGAGTCTGTGTAACAGCTGGGGGTCCTGAGACTCT 186
QY 62 CCTGTGACGCTCTGATTCACCTTTGATGATTAATGCACTGGTCCGACAGCTC 121
DB 187 CCTGTGACGCTCTGATTCACCTTTGATGATTAATGCACTGGTCCGACAGCTC 246
QY 122 CAGGCAAGGGGCTGAGTGGTGGCAGTTATATCATATGATGGAATTAATACTATG 181
DB 247 CAGGCAAGGGGCTGAGTGGTGGCAGTTATATCATATGATGGAATTAATACTATG 306
QY 182 CAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGCAATTCGAAGAACGCTGTATC 241
DB 307 CAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGCAATTCGAAGAACGCTGTATC 366
QY 242 TGCATATGAACAGCTGAGAGTGAAGACACGGCTGTATTACTGTGGGAA----- 294
DB 367 TGCATATGAACAGCTGAGAGTGAAGACACGGCTGTATTACTGTGGGAAAGATCTT 426
QY 295 -----AAGGAAGCTACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCAGACCA 346
DB 427 TGGGGGTTACTTTGATGATGAGTCTGGGGCCAGGGGACCTGTGTCACCGTCTCTCAGCCTCA 486
QY 347 CCAAGGCTCCGATGTGTTCCCTCT 371
DB 487 CCAAGGCTCCGATGTGTTCCCTCT 511

RESULT 5
CD687626 621 bp mRNA linear EST 25-JUN-2003
LOCUS EST4147 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD687626
VERSION CD687626.1 GI:32205644
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 621)
Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.
Transcriptional Gene Expression Profile of Human Nasopharynx
Unpublished (2003)
Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 DongFeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
Location/Qualifiers
1. .621

FEATURES

source

ORIGIN

ORIGIN

ORIGIN

Query Match	74.4%	Score 276.8	DB 5	Length 907
Best Local Similarity	84.5%	Pred. No. 4e-71		
Matches 333	Conservative	0	Mismatches 37	Indels 24
				Gaps 1
QY	2	AGGTGCAGCTGCTGGAGCTGGGGGAGTCGTGTACAGCCTGGGGGGTCCCTGAGACTCT	61	
DB	103	AGGTGCAGCTGTGAATCTGGGGGAGGCGTGTCCAGCCTGGGGGGTCCCTGAGACTCT	162	
QY	62	CCTGTGCAGCCTCTGATTCACCTTTGATGATTAATGCCATCAGCTGGTCCGCCAGGCTC	121	
DB	163	CCTGTGCAGCCTCTGATTCACCTTTGATGATTAATGCCATCAGCTGGTCCGCCAGGCTC	222	
QY	122	CAGGCAGAGGGCTGTGAGTGGGTGSCAGTAAATCATATGATGAGAAAGTAATAATACATAG	181	
DB	223	CAGGCAGAGGGCTGTGAGTGGGTGTCATTTAACGATGATGAGAAAGTAATAATACATAG	282	
QY	182	CAGACTCCGTGAAGGGCCGATTCAACATCTCCAGAGCAATTCACAAGAACCGCTGTATC	241	
DB	283	CAGACTTGTGAAGGGCCGATTCAACATCTCCAGAGCAATTCACAAGAACCGCTGTATC	342	
QY	242	TGCAATATGAACAGCCTGAGACTGAGACACACGGCTGTATTAATCTGTGCCAAAAA----	296	
DB	343	TGCAATATGAACAGCCTGAAACCTGAGGACACGGCTGTATTAATCTGTGCCAAAGATTGCA	402	
QY	297	-----GGAGGCTACTGGGGCAGAGAAACCTGTGACCGCTCT	337	
DB	403	TGTGGGTGATGATGCTCTTTTGACTACTATGGGGCAGAGAAACCTGTGTACCGTCTCT	462	

RESULT 7				
BM914366				
LOCUS				
DEFINITION	BM914366	1001 bp	mRNA	linear
	AGENCOURT	6615562	NIH_MGC_113 Homo sapiens	EST 12-MAR-2007
	5' mRNA sequence.		CDNA clone IMAGE:5480033	

ORGANISM	REFERENCE
Homo sapiens	1 (bases 1 to 1001)
Euryarchaeota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi	
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 1001)				
	NIH-MGC	http://mgc.nci.nih.gov/		
	National Institutes of Health, Mammalian Gene Collection (MGC)			
	Unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgabs@remail.nih.gov			
	Tissue Procurement: Dr. Mark Watson			
	cDNA Library Preparation: Rubin Laboratory			
	Consortium (LNL)			
	Arrayed by: The I.M.A.G.E. Consortium			
	DNA Sequencing by: Agencourt Bioscience Corporation			
	MGSC clone distribution information can be			

http://image.llnl.gov
Plate: LLCM2002 row: d column: 20

High quality sequence stop: 674.

Location/Qualifiers

FEATURES

source

1..1001
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5480035"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 74.4%; Score 276.8; DB 4; Length 1001;

Best Local Similarity 84.5%; Pred. No. 4.1e-71;

Matches 333; Conservative 0; Mismatches 37; Indels 24; Gaps 1;

2 AGGTGAGCTGCTCGAGTCTGGGGAGTGTGGTACAGCCTGGGGGTCCTGAGACTCT 61
|||||
102 AGGTGAGCTGCTGAGTCTGGGGAGTGTGGTACAGCCTGGGGGTCCTGAGACTCT 161
62 CCTGTGACGCTCTGATTCACCTTTGATGATTAATGACATGACCTGGGTCGGCAGGCTC 121
|||||
162 CCTGTGACGCTCTGATTCACCTTTGATGATTAATGACATGACCTGGGTCGGCAGGCTC 221
122 CAGGCAAGGGGCTGGAGTGGTGGCAGTATATCATATGATGAGTAATTAATTAATCTATG 181
|||||
222 CAGGCAAGGGGCTGGAGTGGTGGCAGTATATCATATGATGAGTAATTAATTAATCTATG 281
182 CAGACTCCGCTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGAACAGCCTGATC 241
|||||
282 CAGACTCCGCTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGAACAGCCTGATC 341
242 TGCATTAATGAACAGCCTGAGAGCTGAGAGACAGGCTGTGATTAATCTGTGCGAAAAA 296
|||||
342 TGCATTAATGAACAGCCTGAGAGCTGAGAGACAGGCTGTGATTAATCTGTGCGAAAAA 401
297 -----GGAAGCTACTGAGGGGCGGAGGAAACCTGTGTCACCTCTCTCT 337
|||||
402 TGTGGGGTGAATGATGCTCTTTTGTACTTACGTGGGGCCAGGAAACCTGTGTCACCTCTCT 461
Db 402 TGTGGGGTGAATGATGCTCTTTTGTACTTACGTGGGGCCAGGAAACCTGTGTCACCTCTCT 461
Qy 338 CAGCACCACCAAGGCTCCGATGTGTTCCTCT 371
1 |||||
Db 462 CAGCCTCCACCAAGGGCCATCGTCTTCCCT 495

RESULT 8 BG340648 678 bp mRNA linear EST 27-FEB-2001

LOCUS BG340648 602462226F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4574935 5',

DEFINITION mRNA sequence.

ACCESSION BG340648

VERSION BG340648.1 GI:13147086

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE NIH-MGC http://mgi.nci.nih.gov/

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI285 row: d column: 08
High quality sequence stop: 666.

Location/Qualifiers

FEATURES

source

1..678
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4574935"
/issue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 73.7%; Score 274.2; DB 4; Length 678;

Best Local Similarity 95.6%; Pred. No. 2.2e-70;

Matches 282; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

2 AGGTGAGCTGCTCGAGTCTGGGGAGTGTGGTACAGCCTGGGGGTCCTGAGACTCT 61
|||||
130 AGGTGAGCTGCTGAGTCTGGGGAGTGTGGTACAGCCTGGGGGTCCTGAGACTCT 189
62 CCTGTGACGCTCTGATTCACCTTTGATGATTAATGACATGACCTGGGTCGGCAGGCTC 121
|||||
190 CCTGTGACGCTCTGATTCACCTTTGATGATTAATGACATGACCTGGGTCGGCAGGCTC 249
122 CAGGCAAGGGGCTGGAGTGGTGGCAGTATATCATATGATGAGTAATTAATTAATCTATG 181
|||||
250 CAGGCAAGGGGCTGGAGTGGTGGCAGTATATCATATGATGAGTAATTAATTAATCTATG 309
182 CAGACTCCGCTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGAACAGCCTGATC 241
|||||
310 CAGACTCCGCTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGAACAGCCTGATC 369
242 TGCATTAATGAACAGCCTGAGAGCTGAGAGACAGGCTGTGATTAATCTGTGCGAAAAA 296
|||||
370 TGCATTAATGAACAGCCTGAGAGCTGAGAGACAGGCTGTGATTAATCTGTGCGAAAAA 424
Db 370 TGCATTAATGAACAGCCTGAGAGCTGAGAGACAGGCTGTGATTAATCTGTGCGAAAAA 424

RESULT 9

LOCUS BG342203

DEFINITION 788 bp mRNA linear EST 27-FEB-2001

ACCESSION BG342203

VERSION BG342203.1 GI:13148641

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE NIH-MGC http://mgi.nci.nih.gov/

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLCM1287 row: m column: 20

High quality sequence stop: 687.

FEATURES

source

Location/Qualifiers

1..788

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4575931"

/tissue_type="Primary B-cells from tonsils (cell line)"

/lab_host="DH10B (phage-resistant)"

/clone_idb="NIH_MGC_48"

/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Size-selected >500bp

for average insert size 1.8kb. Library constructed by Ling

Hong in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."

ORIGIN

Query Match

73.7%; Score 274.2; DB 4; Length 788;

Best Local Similarity 95.6%; Pred. No. 2.3e-70;

Matches 282; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2 AGGTGACAGCTGCTCGAGTCTGGGGAGTGGTACAGCTGGGGGCTCCCTGAGACTCT 61

DB 129 AGGTGACAGCTGCTGGAGTCTGGGGAGGCTGCTCCAGCTGGAGGTCCTGAGACTCT 188

QY 62 CTTGTCAGGCTCTGGAATTCACCTTGATGATTATGCAATGACCTGGTCCGACAGCTC 121

DB 189 CTTGTCAGGCTCTGGAATTCACCTTGATGATTATGCAATGACCTGGTCCGACAGCTC 248

QY 122 CAGGCAAGGGGCTGGAGTGGGTCAGTTATATCATATGATGAGAAATTAATTAATATG 181

DB 249 CAGGCAAGGGGCTGGAGTGGGTCAGTTATATCATATGATGAGAAATTAATTAATATG 308

QY 182 CAGACTCCGTCGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGAACAGCTGTATC 241

DB 309 CAGACTCCGTCGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGAACAGCTGTATC 368

QY 242 TGCATATGAACAGCTGAGAGCTGAGAGACACGGCTGTATTACTGTGCGAAAAA 296

DB 369 TGCATATGAACAGCTGAGAGCTGAGAGACACGGCTGTATTACTGTGCGAAAAA 423

RESULT 10

BG759649 870 bp mRNA linear EST 15-MAY-2001

LOCUS 602713342F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:485338 5',

DEFINITION mRNA sequence.

ACCESSION BG759649

VERSION BG759649.1 GI:114070302

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 870)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLCM1699 row: d column: 11

High quality sequence stop: 764.

FEATURES

source

Location/Qualifiers

1..870

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:485338"

/tissue_type="Primary B-cells from tonsils (cell line)"

/lab_host="DH10B (phage-resistant)"

/clone_idb="NIH_MGC_48"

/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Size-selected >500bp

for average insert size 1.8kb. Library constructed by Ling

Hong in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."

ORIGIN

Query Match

73.7%; Score 274.2; DB 4; Length 870;

Best Local Similarity 95.6%; Pred. No. 2.4e-70;

Matches 282; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2 AGGTGACAGCTGCTCGAGTCTGGGGAGTGGTACAGCTGGGGGCTCCCTGAGACTCT 61

DB 130 AGGTGACAGCTGCTGGAGTCTGGGGAGGCTGCTCCAGCTGGAGGTCCTGAGACTCT 189

QY 62 CTTGTCAGGCTCTGGAATTCACCTTGATGATTATGCAATGACCTGGTCCGACAGCTC 121

DB 190 CTTGTCAGGCTCTGGAATTCACCTTGATGATTATGCAATGACCTGGTCCGACAGCTC 249

QY 122 CAGGCAAGGGGCTGGAGTGGGTCAGTTATATCATATGATGAGAAATTAATTAATATG 181

DB 250 CAGGCAAGGGGCTGGAGTGGGTCAGTTATATCATATGATGAGAAATTAATTAATATG 309

QY 182 CAGACTCCGTCGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGAACAGCTGTATC 241

DB 310 CAGACTCCGTCGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGAACAGCTGTATC 369

QY 242 TGCATATGAACAGCTGAGAGCTGAGAGACACGGCTGTATTACTGTGCGAAAAA 296

DB 370 TGCATATGAACAGCTGAGAGCTGAGAGACACGGCTGTATTACTGTGCGAAAAA 424

RESULT 11

BF663281 964 bp mRNA linear EST 21-DEC-2000

LOCUS 602144406F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297849 5',

DEFINITION mRNA sequence.

ACCESSION BF663281

VERSION BF663281.1 GI:11937163

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 964)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLCM1152 row: k column: 02
High quality sequence stop: 693.
Location/Qualifiers

FEATURES

source

1. .964
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4297849"
/issue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;
Site:2: EcoRI; cDNA made by oligo-dt priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

ORIGIN

Query Match 73.7%; Score 274.2; DB 2; Length 964;
Best Local Similarity 95.6%; Pred. No. 2.4e-70;
Matches 282; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2 AGGTGACGCTGCTCGAGTCTGGGGAGTGTGTGTACAGCTGGGGGTCCTTGAGACTCT 61
DB 130 AGGTGACGCTGCTGGAGTCTGGGGAGGAGGTGTGTCCAGCTGGAGAGTCCCTGAGACTCT 189
QY 62 CCTGTGCAACCTCTGATTCACCTTTGATGATTAATGCACTGCGTCCGACAGCTC 121
DB 190 CCTGTGCAACCTCTGATTCACCTTTGATGATTAATGCACTGCGTCCGACAGCTC 249
QY 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAAATTAATACATG 181
DB 250 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGAGAAATTAATACATG 309
QY 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 241
DB 310 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 369
QY 242 TGCATATGAACAGCTGAGAGCTGAGAGCAACGCGCTGTATTACTGTGGAAAAA 296
DB 370 TGCATATGAACAGCTGAGAGCTGAGAGCAACGCGCTGTATTACTGTGGAAAAA 424

RESULT 12

BP974524 991 bp mRNA linear EST 22-JAN-2001
LOCUS BP974524
DEFINITION 602243430F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4334719 5',
mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 991)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Plate: LLCM1204 row: k column: 08
High quality sequence stop: 688.
Location/Qualifiers

FEATURES

source

1. .991
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4334719"
/issue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;
Site:2: EcoRI; cDNA made by oligo-dt priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

ORIGIN

Query Match 73.7%; Score 274.2; DB 2; Length 991;
Best Local Similarity 95.6%; Pred. No. 2.4e-70;
Matches 282; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2 AGGTGACGCTGCTCGAGTCTGGGGAGTGTGTGTACAGCTGGGGGTCCTTGAGACTCT 61
DB 130 AGGTGACGCTGCTGGAGTCTGGGGAGGAGGTGTGTCCAGCTGGAGAGTCCCTGAGACTCT 189
QY 62 CCTGTGCAACCTCTGATTCACCTTTGATGATTAATGCACTGCGTCCGACAGCTC 121
DB 190 CCTGTGCAACCTCTGATTCACCTTTGATGATTAATGCACTGCGTCCGACAGCTC 249
QY 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAAATTAATACATG 181
DB 250 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGAGAAATTAATACATG 309
QY 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 241
DB 310 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 369
QY 242 TGCATATGAACAGCTGAGAGCTGAGAGCAACGCGCTGTATTACTGTGGAAAAA 296
DB 370 TGCATATGAACAGCTGAGAGCTGAGAGCAACGCGCTGTATTACTGTGGAAAAA 424

RESULT 13

BP663436 1010 bp mRNA linear EST 21-DEC-2000
LOCUS BP663436
DEFINITION 602144593F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297847 5',
mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1010)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Plate: LLCM1152 row: j column: 24

FEATURES
source
High quality sequence stop: 695.
Location/Qualifiers
1. .1010
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4297847"
/issue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 73.7%; Score 274.2; DB 2; Length 1010;
Best Local Similarity 95.6%; Pred. No. 2.4e-70;
Matches 282; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2 AGGTGACAGCTGCTGAGTCTGGGGAGTGTGTACAGCTGGGGGCTCCCTGAGACTCT 61
DB 130 AGGTGACAGCTGCTGAGTCTGGGGAGTGTGTACAGCTGGGGGCTCCCTGAGACTCT 189
QY 62 CCTGTGACAGCTCTGAGTCTGAGTCTGGGGAGTGTGTACAGCTGGGGGCTCCCTGAGACTCT 121
DB 190 CCTGTGACAGCTCTGAGTCTGAGTCTGGGGAGTGTGTACAGCTGGGGGCTCCCTGAGACTCT 249
QY 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAGTAATAAATATATG 181
DB 250 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAGTAATAAATATATG 309
QY 182 CAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGCAATTCAGAGACAGCTGTATC 241
DB 310 CAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGCAATTCAGAGACAGCTGTATC 369
QY 242 TGCAGATGAACAGCTGAGAGTGAAGACAGGCTGTATTAATCTGTGCGAATA 296
DB 370 TGCAGATGAACAGCTGAGAGTGAAGACAGGCTGTATTAATCTGTGCGAATA 424

RESULT 14
BG755572 846 bp mRNA linear EST 15-MAY-2001
LOCUS 60271625F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4856628 5',
DEFINITION mRNA sequence.
ACCESSION BG755572
VERSION BG755572.1 GI:14066225
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 846)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LNCM1707 row: m column: 13
High quality sequence stop: 752.

FEATURES
source
Location/Qualifiers
1. .846
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4856628"
/issue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 73.4%; Score 273.2; DB 4; Length 846;
Best Local Similarity 95.6%; Pred. No. 4.7e-70;
Matches 281; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2 AGGTGACAGCTGCTGAGTCTGGGGAGTGTGTACAGCTGGGGGCTCCCTGAGACTCT 61
DB 130 AGGTGACAGCTGCTGAGTCTGGGGAGTGTGTACAGCTGGGGGCTCCCTGAGACTCT 189
QY 62 CCTGTGACAGCTCTGAGTCTGAGTCTGGGGAGTGTGTACAGCTGGGGGCTCCCTGAGACTCT 121
DB 190 CCTGTGACAGCTCTGAGTCTGAGTCTGGGGAGTGTGTACAGCTGGGGGCTCCCTGAGACTCT 249
QY 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAGTAATAAATATATG 181
DB 250 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAGTAATAAATATATG 309
QY 182 CAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGCAATTCAGAGACAGCTGTATC 241
DB 310 CAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGCAATTCAGAGACAGCTGTATC 369
QY 242 TGCAGATGAACAGCTGAGAGTGAAGACAGGCTGTATTAATCTGTGCGAATA 295
DB 370 TGCAGATGAACAGCTGAGAGTGAAGACAGGCTGTATTAATCTGTGCGAATA 423

RESULT 15
BG756211 912 bp mRNA linear EST 15-MAY-2001
LOCUS 602713521F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853837 5',
DEFINITION mRNA sequence.
ACCESSION BG756211
VERSION BG756211.1 GI:14066864
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 912)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LNCM1700 row: i column: 06
High quality sequence stop: 889.
Location/Qualifiers

FEATURES


```
source
1. .912
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4853837"
/issue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/notes="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
```

ORIGIN

```
Query Match      73.3%; Score 272.6; DB 4; Length 912;
Best Local Similarity 95.3%; Pred. No. 7.1e-70;
Matches 281; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY      2 AGGTGAGCTGCTCGAGTCTGGGGAGTGGTGTACAGCCTGGGGGTCCTGAGACTCT 61
      |||
Db      121 AGGTGAGCTGCTGGAGTCTGGGGAGGCGTGTCCAGCTGGAGAGTCCCTGAGACTCT 180

QY      62 CCTGTGAGCCTCTGGAATTCACCTTTGATGATTATGSCCATGCACTGGGTCCGCCAGGCTC 121
      |||
Db      181 CCTGTGAGCCTCTGGAATTCACCTTCAGTATTATGGCATGAAGTGGGTCCGCCAGGCTC 240

QY      122 CAGGCAAGGGGCTGGAGTGGTGGCAGTTATCATATGATGGAAGTAATAATACTATG 181
      |||
Db      241 CAGGCAAGGGGCTGGAGTGGTGGCAGTTATCATATGATGGAAGTAATAATACTATG 300

QY      182 CAGACTCCGTTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAGAAACACGCTGTATC 241
      |||
Db      301 CAGACTCCGTTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAGAAACACGCTGTATC 360

QY      242 TGCATAATGAACAGCCTGAGAGCTGAGAGACACGGCTGTGATTATCTGTGCGAAAAA 296
      |||
Db      361 TGCATAATGAACAGCCTGAGAGCTGAGAGACACGGCTGTGATTATCTGTGCGAAAAA 415
```

Search completed: December 7, 2004, 11:13:50
Job time : 2171.93 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 02:37:53 ; Search time 1815.78 Seconds
(without alignments)
8360.047 Million cell updates/sec

Title: US-09-403-107-147

Sequence: 1 gacgtccagatgacccagtc.....ggacacgactggacattcaa 321

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 segs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenBank: *
1: gb_ba: *
2: gb_ncg: *
3: gb_in: *
4: gb_cm: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	321	100.0	321	6	AB4380 Sequence 14
2	321	100.0	321	6	BD075296 Novel met
3	321	100.0	1630	6	BD222938 Heteromim
4	321	100.0	1630	6	BD222939 Heteromim
5	321	100.0	1630	6	AX023365 Sequence
6	321	100.0	1630	6	AX023367 Sequence
7	260.2	81.1	321	6	AB4374 Sequence 14
8	260.2	81.1	321	6	AX003761 Sequence
9	260.2	81.1	321	6	BD075293 Novel met
10	260.2	81.1	321	6	BD139668 A novel m
11	245.8	76.6	324	6	BD187178 Human-tyr
12	245.8	76.6	324	6	BD187179 Human-tyr
13	244.2	76.1	339	9	AB006842 Homo sapi
14	244.2	76.1	342	6	BD097614 Anticbody
15	242.6	75.6	321	6	BD097618 Anticbody
16	242.6	75.6	814	9	AB064076 Homo sapi
17	241	75.1	315	9	HSFA82VL Y08148 H.sapiens m
18	240.8	75.0	318	12	AF044455 Synthetic
19	240.8	75.0	321	6	AR160977 Sequence

20	239.4	74.6	339	9	AB006846
21	237.8	74.1	324	6	AX112586
22	237.8	74.1	735	6	CQ832185 Sequence
23	237	73.8	324	9	AB095290 Homo sapi
24	236.2	73.6	321	6	A29589
25	236.2	73.6	324	12	AF538596
26	236.2	73.6	642	9	AB095273
27	236.2	73.6	1000	9	HSVK01
28	235.6	73.4	324	9	HSIG111
29	234.6	73.1	612	9	HUMIGRAE
30	234.6	73.1	642	9	AB030640
31	234.4	73.0	936	6	BD248703
32	233	72.6	324	6	HSVTERP
33	233	72.6	450	9	AF103775
34	232.8	72.5	917	6	BD248694
35	231.8	72.2	384	9	HSBOM016
36	231.4	72.1	324	9	AB063929
37	231.4	72.1	333	6	BD097236
38	231.4	72.1	346	9	HSQIB6TGK
39	231.4	72.1	388	9	HSAB48508
40	231.4	72.1	720	6	CQ761230
41	231.4	72.1	720	6	CQ840583
42	231.4	72.1	720	6	AR476229
43	231.4	72.1	720	6	AX740176
44	231.4	72.1	720	6	BD077368
45	231.4	72.1	761	9	AB064051

ALIGNMENTS

RESULT 1	AB4380	Sequence 147 from Patent WO9846645.	321 bp	DNA	linear	PAT 21-JAN-2000
LOCUS	AB4380					
DEFINITION	Sequence 147 from Patent WO9846645.					
ACCESSION	AB4380					
VERSION	AB4380.1	GI:6733303				
KEYWORDS	unidentified					
SOURCE	unidentified					
ORGANISM	unclassified.					
REFERENCE	1 (bases 1 to 321)					
AUTHORS	Kuifer, P. and Raum, T.					
TITLE	NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN RECEPTORS AND					
JOURNAL	US5 THEREOF					
FEATURES	Patent: WO 9846645-A 147 22-OCT-1998;					
source	KUFEER PETER (DE); RAUM TOBIAS (DE)					
	location/Qualifiers					
	1..321					
	/organism="unidentified"					
	/mol_type="unassigned DNA"					
	/db_xref="taxon:32644"					
	<1..>321					
	/note="unnamed protein product"					
	/codon_start=1					
	/protein_id="CAB69290.1"					
	/db_xref="GI:6733304"					
	/translation="ELQMTQSPSSLSASVGRVITTCRAQSISLYINWYQKPCOP					
	KLLIYVASTRESGVPRFSGSISGTYTLTISLQPEDPATVYCCQSDSLPIFGQT					
	RDIQ"					
ORIGIN						
Query Match	100.0%; Score 321; DB 6; Length 321;					
Best Local Similarity	100.0%; Pred. No. 2,3e-97;					
Matches	321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1 GAGCTTCAGATGACCCAGTCTCATCTCCCTGTCGATCTCTAGAGACAGAGTCACC					60
DB	1 GAGCTTCAGATGACCCAGTCTCATCTCCCTGTCGATCTCTAGAGACAGAGTCACC					60
QY	61 ATCACTTCCGGGCGGAGTCAGAGCATTTAGAGCATTTAAATTGATACGAGAACA					120
DB	61 ATCACTTCCGGGCGGAGTCAGAGCATTTAGAGCATTTAAATTGATACGAGAACA					120

QY 121 GGAAGCTCTCTTAAGTGTCTATTACTGGGCACTTACCAGGAATCCGGGGTCCCTGAC 180
DB 121 GGAAGCTCTCTTAAGTGTCTATTACTGGGCACTTACCAGGAATCCGGGGTCCCTGAC 180
QY 181 CGATTGAGGGGAGGATCTGGGCAAAATTACACTCTGACATGAGAGCTGAGAGCT 240
DB 181 CGATTGAGGGGAGGATCTGGGCAAAATTACACTCTGACATGAGAGCTGAGAGCT 240
QY 241 GAAAGATTTGGCTACTTCTTTGTCAACAGTGTGACAGTTTGGCGATCACTTGGCCAA 300
DB 241 GAAAGATTTGGCTACTTCTTTGTCAACAGTGTGACAGTTTGGCGATCACTTGGCCAA 300
QY 301 GGGACAGCACTGAGCAATTCOA 321
DB 301 GGGACAGCACTGAGCAATTCOA 321

RESULT 2
BD075296 321 bp DNA linear PAT 27-AUG-2002
LOCUS BD075296
DEFINITION Novel method for the production of anti-human antigen receptors and uses thereof.
ACCESSION BD075296
VERSION BD075296.1 GI:22620899
KEYWORDS JP 2001519824-A/25.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 321)
AUTHORS Kufer, P. and Raum, T.
TITLE Novel method for the production of anti-human antigen receptors and uses thereof
JOURNAL Patent: JP 2001519824-A 25 23-OCT-2001;
MICROMET AG
COMMENT OS Homo sapiens (human)
PN JP 2001519824-A/25
PD 23-OCT-2001 JP 1998543494
PR 14-APR-1998 JP 97106109.8
PI PETER KUFER, TOBIAS RAUM
PC C07K16/00, C07K16/30, A61K39/395
CC Novel method for the production of anti-human antigen CC
receptors and uses
CC therect
FH Key
FT CDS Location/Qualifiers
1..321
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 321; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 2.3e-97;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 181 CGATTGAGGGGAGGATCTGGGCAAAATTACACTCTGACATGAGAGCTGAGAGCT 240
QY 241 GAAAGATTTGGCTACTTCTTTGTCAACAGTGTGACAGTTTGGCGATCACTTGGCCAA 300
DB 241 GAAAGATTTGGCTACTTCTTTGTCAACAGTGTGACAGTTTGGCGATCACTTGGCCAA 300
QY 301 GGGACAGCACTGAGCAATTCOA 321
DB 301 GGGACAGCACTGAGCAATTCOA 321

RESULT 3
BD222938 1630 bp DNA linear PAT 17-JUL-2003
LOCUS BD222938
DEFINITION Heteromabinbodies.
ACCESSION BD222938
VERSION BD222938.1 GI:33032708
KEYWORDS JP 2002521053-A/32.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1630)
AUTHORS Kufer, P., Dreier, T., Baeuerle, P.A., Borschert, K. and Zettl, F.
TITLE Heteromabinbodies
JOURNAL Patent: JP 2002521053-A 32 16-JUL-2002;
MICROMET AG
COMMENT OS Homo sapiens (human)
PN JP 2002521053-A/32
PD 16-JUL-2002
PR 28-JUL-1998 JP 2000562401
PI PETER KUFER, TORSTEN DREIER, PATRICK A BAEUERLE, KATRIN BORSCHERT,
PI FLORIAN ZETTL
PC C12N15/09, A61K35/76, A61K38/00, A61K38/21, A61P35/00, A61P35/02,
PC C07K19/00,
PC C12N5/10, C12P21/02, G01N33/53, G01N33/53//C12N5/10, C12R1:91),
PC (C12P21/02, C12R1:91), C12N15/00, C12N5/00, A61K37/02, A61K37/66,
PC (C12N5/00, C12R1:91)
CC Heteromabinbodies
FH Key
FT CDS Location/Qualifiers
1..1630
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 321; DB 6; Length 1630;
Best Local Similarity 100.0%; Pred. No. 2.5e-97;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 336 GAAGATTTTGCTACTTACTTTTGTCAACAGCTGTGACAGTTTGGCGATCACCCTTGGGCCAA 395
QY 301 GGGACACGACTGGACATTCAA 321
396 GGGACACGACTGGACATTCAA 416

RESULT 4
BD222939
LOCUS BD222939 1630 bp DNA linear PAT 17-JUL-2003
DEFINITION Heteromniobodies.
ACCESSION BD222939
VERSION BD222939.1 GI:33032709
KEYWORDS JP 2002521053-A/33.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Kufner, P., Dreier, T., Baeuerle, P.A., Borschert, K. and Zettl, F.
JOURNAL Heteromniobodies
Patent: JP 2002521053-A 33 16-JUL-2002;
MICROMET AG

COMMENT
OS Homo sapiens (human)
PN JP 2002521053-A/33
PD 16-JUL-2002
PF 28-JUL-1999 JP 2000562401
PR 28-JUL-1998 EP 98114082.5
PI PETER KUFNER, TORSTEN DREIER, PATRICK A BAEUERLE, KATRIN BORSCHERT,
BORSCHERT,
PI FLORIAN ZETTL
PC C12N15/09, A61K35/76, A61K38/00, A61K38/21, A61P35/00, A61P35/02,
PC C07K13/00,
PC C12N5/10, C12P21/02, G01N33/53, G01N33/53// (C12N5/10, C12R1.91),
PC (C12P21/02, C12R1.91), C12N15/00, C12N5/00, A61K37/02, A61K37/66,
PC (C12N5/00, C12R1.91)
CC Heteromniobodies
FT Key Location/Qualifiers
CDS (39)..(1610).

FEATURES
source
1..1630
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 321; DB 6; Length 1630;
Best Local Similarity 100.0%; Pred. No. 2.5e-97;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTGTGATCTGTAGAGACAGAGTCACC 60
DB 96 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTGTGATCTGTAGAGACAGAGTCACC 155
QY 61 ATCACTTGGCCGGGCAAGTCAAGACATTAAGCACTATTAAATTGGTATGACGAGAAACA 120
DB 156 ATCACTTGGCCGGGCAAGTCAAGACATTAAGCACTATTAAATTGGTATGACGAGAAACA 215
QY 121 GAGACGCTCTTAAGCTGTCTATTACTGGGATCTACCCGGGAAATCCGGGGTCCCTGAC 180
DB 216 GAGACGCTCTTAAGCTGTCTATTACTGGGATCTACCCGGGAAATCCGGGGTCCCTGAC 275
QY 181 CGATTCAAGGGGAGTGAATCTGGGACAAATTACACTTCACATCAGACAGCTTGAGCCT 240
DB 276 CGATTCAAGGGGAGTGAATCTGGGACAAATTACACTTCACATCAGACAGCTTGAGCCT 335
QY 241 GAAGATTTTGCTACTTACTTTTGTCAACAGCTGTGACAGTTTGGCGATCACCCTTGGGCCAA 300
DB 336 GAAGATTTTGCTACTTACTTTTGTCAACAGCTGTGACAGTTTGGCGATCACCCTTGGGCCAA 395
QY 301 GGGACACGACTGGACATTCAA 321
396 GGGACACGACTGGACATTCAA 416

Db 396 GGGACACGACTGGACATTCAA 416

RESULT 5
AX023365
LOCUS AX023365 1630 bp DNA linear PAT 15-SEP-2000
DEFINITION Sequence 36 from Patent WO0006605.
ACCESSION AX023365
VERSION AX023365.1 GI:10183777
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Kufner, P., Zettl, F., Dreier, T., Baeuerle, P.A. and Borschert, K.
JOURNAL Heteromniobodies
Patent: WO 0006605-A 36 10-SEP-2000;
KUFNER PETER (DE) ; ZETTL FLORIAN (DE) ; DREIER TORSTEN (DE) ;
BAEUEERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GRS FUER
BIOMEDIZINIS (DE)
Location/Qualifiers

FEATURES
source
1..1630
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
39..1610
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC08835.1"
/db_xref="GI:10183778"

CDS
1
translation="MGMSCITLFLVATATGVSLEQMTQSPSSLSASVGRVTTTCRA
SOSISSYLMVYQKQKQPEPKLIYVASTRESVPRFSGSEGTNVTLLTISLQEPD
ATPCQOSDLPITFGQGTDLDIQGGGGGGGGGGSEVQLLSGGGVVQPGSIR
LSAASGFFSFGYGNHWROAPKGLBMYAVISYGSNKYVADSVKGRPTIRDSKXN
TLYLQMSNIRADDTAVVYCAKMGWSGMRPYVYVGGQVMDVGGCTTVTSVSGTLDGTT
HTASKGSPVPLPASPSSKTSSTGTLALGLVADYTPPEPVVSMNGALTSVHTPPAV
LQSSGLVLSLVVTVPSVSLGTQYICNVNHRPSNTKVKVPEKSCDTSGGGSGAP
ASPSPTQPMWENAVAIQEARLLNLSRDTAEMNVEVISEMDLQPTCLQTELE
LYKQGLRSITLTKGRLPTLWMAISHYKQHCPTPETSQATQIITFESFKENLKDFLIVIP
FDCEPVEQHHHHHHH"

ORIGIN
Query Match 100.0%; Score 321; DB 6; Length 1630;
Best Local Similarity 100.0%; Pred. No. 2.5e-97;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTGTGATCTGTAGAGACAGAGTCACC 60
DB 96 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTGTGATCTGTAGAGACAGAGTCACC 155
QY 61 ATCACTTGGCCGGGCAAGTCAAGACATTAAGCACTATTAAATTGGTATGACGAGAAACA 120
DB 156 ATCACTTGGCCGGGCAAGTCAAGACATTAAGCACTATTAAATTGGTATGACGAGAAACA 215
QY 121 GAGACGCTCTTAAGCTGTCTATTACTGGGATCTACCCGGGAAATCCGGGGTCCCTGAC 180
DB 216 GAGACGCTCTTAAGCTGTCTATTACTGGGATCTACCCGGGAAATCCGGGGTCCCTGAC 275
QY 181 CGATTCAAGGGGAGTGAATCTGGGACAAATTACACTTCACATCAGACAGCTTGAGCCT 240
DB 276 CGATTCAAGGGGAGTGAATCTGGGACAAATTACACTTCACATCAGACAGCTTGAGCCT 335
QY 241 GAAGATTTTGCTACTTACTTTTGTCAACAGCTGTGACAGTTTGGCGATCACCCTTGGGCCAA 300
DB 336 GAAGATTTTGCTACTTACTTTTGTCAACAGCTGTGACAGTTTGGCGATCACCCTTGGGCCAA 395
QY 301 GGGACACGACTGGACATTCAA 321
396 GGGACACGACTGGACATTCAA 416

RESULT 6

AX023367 AX023367 1630 bp DNA linear PAT 15-SEP-2000
LOCUS
DEFINITION Sequence 38 from Patent WO0006505.
ACCESSION AX023367
VERSION AX023367.1 GI:10183779
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS Kufer, P., Zetli, F., Dreier, T., Baeuerle, P. A. and Borschert, K.
TITLE Heteromimodies
JOURNAL Patent: WO 0006505-A 38 10-FEB-2000;
KUFER PETER (DE) ; ZETTL FLORIAN (DE) ; DREIER TORSTEN (DE) ;
BAEUEERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GBS FUER
BIOMEDIZINIS (DE)
FEATURES
source
1. 1630
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
39..1613
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC08836.1"
/db_xref="GI:10183780"
/translation="MGMSCTILFLVATATGVHSELQMTGPSLSASVGDRTVITTCRA
SGSISLYNWYQKPGPKLILYMASTESGVPDFSGSEGTNTLLTSLIOBEDP
ATYFCOSDLPITFGQGRLLIOGGSGGGSGEVLLEGGGCVVOPGSLR
LSCAASGFTFSSGMMHWROAPBKGLEWAVISYDSNNKYADSVYGRRTIRDSKN
TLYLQNSLRAPETAVYCAKMGSGSPRYVYGMVDCGCTVTVSSSGRLDIT
HRTVAPSVFTFPPSDEQKSGTASVCLNNFYREKRVQKNDNALQSGNSQESV
TEQDSKOSTYSLSTLLSKADYERKHYACEVTHQGLSPVTKSFNRSGGGGSA
PISSSTYKTLQLEHLILDLOMLNGINNYKPKLITMLTFPKYKKAETELKHLOCL
EELKPLEEVLNLAOSKFNHRLPRDLISINIVLIEKSGSETFMCEYADETATIVER
LNRWITFCQSIISTLT"

ORIGIN
Query Match 100.0%; Score 321; DB 6; Length 1630;
Best Local Similarity 100.0%; Pred. No. 2.5e-97;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGCTCCAGATGACCCAGTCTCATCTCCCTGCTGACATCTAGAGAGAGATCACC 60
DB 96 GAGCTCCAGATGACCCAGTCTCATCTCCCTGCTGACATCTAGAGAGAGATCACC 155
QY 61 ATCACTTGCAGGCGCAAGTCAAGACATTAAGCTATTAAATTGTATGACAGAAACCA 120
DB 156 ATCACTTGCAGGCGCAAGTCAAGACATTAAGCTATTAAATTGTATGACAGAAACCA 215
QY 121 GGAAGCCTCTTAAGTCTCATTTAAGTGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
DB 216 GGAAGCCTCTTAAGTCTCATTTAAGTGGCATCTACCCGGGAATCCGGGGTCCCTGAC 275
QY 181 CGATTGAGGCGGCGAATCTGGGCAAAATTAACCTCAACATCAGACGCGCGAGCCT 240
DB 276 CGATTGAGGCGGCGAATCTGGGCAAAATTAACCTCAACATCAGACGCGCGAGCCT 335
QY 241 GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCGATCACTTGGCCAA 300
DB 336 GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCGATCACTTGGCCAA 395
QY 301 GGGACACGACTGGACATTCAA 321
DB 396 GGGACACGACTGGACATTCAA 416
RESULT 7
LOCUS A84374 321 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 141 from Patent WO9846645.
ACCESSION A84374

VERSION A84374.1 GI:6733297
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 321)
AUTHORS Kufer, P. and Raum, T.
TITLE NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN RECEPTORS AND
JOURNAL USES THEREOF
PATENT: WO 9846645-A 141 22-OCT-1998;
KUFER PETER (DE) ; RAUM TOBIAS (DE)
FEATURES
source
1. 321
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
<1..>321
/note="unnamed protein product"
/codon_start=1
/protein_id="CAB69287.1"
/db_xref="GI:6733298"
/translation="ELQMTGPSLSASVGDRTVITTCRTSGSISLYNWYQKPGPP
KLIYMASTRSGVPDFRSGSGSGTDFLLTITSLIQBEDSATYCOQSYDIPYTGQGT
KLEIK"

ORIGIN
Query Match 81.1%; Score 260.2; DB 6; Length 321;
Best Local Similarity 88.2%; Pred. No. 1e-76;
Matches 283; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 1 GAGCTCCAGATGACCCAGTCTCATCTCCCTGCTGATCTGTAGAGACAGATCACC 60
DB 1 GAGCTCCAGATGACCCAGTCTCATCTCCCTGCTGATCTGTAGAGACAGATCACC 60
QY 61 ATCACTTGCAGGCGCAAGTCAAGACATTAAGCTATTAAATTGTATGACAGAAACCA 120
DB 61 ATCACTTGCAGGCGCAAGTCAAGACATTAAGCTATTAAATTGTATGACAGAAACCA 120
QY 121 GGAAGCCTCTTAAGTCTCATTTAAGTGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
DB 121 GGAAGCCTCTTAAGTCTCATTTAAGTGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
QY 181 CGATTGAGGCGGCGAATCTGGGCAAAATTAACCTCAACATCAGACGCGCGAGCCT 240
DB 181 CGATTGAGGCGGCGAATCTGGGCAAAATTAACCTCAACATCAGACGCGCGAGCCT 240
QY 241 GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCGATCACTTGGCCAA 300
DB 241 GAAGATTTTGTACTTACTTACTTTTGTCAACAGTCTGACAGTTTGGCGATCACTTGGCCAA 300
QY 301 GGGACACGACTGGACATTCAA 321
DB 301 GGGACACGACTGGACATTCAA 321
RESULT 8
LOCUS AX003761 321 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 55 from Patent WO9925818.
ACCESSION AX003761
VERSION AX003761.1 GI:9927567
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS Kufer, P. and Raum, T.
TITLE Method of identifying binding site domains that retain the capacity
JOURNAL of binding to an epitope
PATENT: WO 9925818-A 55 27-MAY-1999;
KUFER PETER (DE) ; RAUM TOBIAS (DE)
FEATURES
Location/Qualifiers

source

1..321
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 81.1%; Score 260.2; DB 6; Length 321;
Best Local Similarity 88.2%; Pred. No. 1e-76;
Matches 283; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTCTGATCTGTAGAGACAGAGTACC 60
DB 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTCTGATCTGTAGAGACAGAGTACC 60
QY 61 ATACTTTGCCGGCAAGTCAAGACATTAGACGCTATTAAATTGGTATACGCAAAACCA 120
DB 61 ATACTTTGCCGGCAAGTCAAGACATTAGACGCTATTAAATTGGTATACGCAAAACCA 120
QY 121 GGACAGCTCTTAAGCTGCTCATTTTCTGGGCACTTACCGGGAAATCCGGGGTCCCTGAC 180
DB 121 GGACAGCTCTTAAGCTGCTCATTTTCTGGGCACTTACCGGGAAATCCGGGGTCCCTGAC 180
QY 181 CGATTGAGCGGCGAGTGAATCTGGGCAAAATTACACTCTACATCAGACAGCTGACGCT 240
DB 181 CGATTGAGCGGCGAGTGAATCTGGGCAAAATTACACTCTACATCAGACAGCTGACGCT 240
QY 241 GAAGATTTTGTCTACTTACTTTTGTCAACAGTCTGACAGATTGCGCATCCGTCGACCA 300
DB 241 GAAGATTTTGTCTACTTACTTTTGTCAACAGTCTGACAGATTGCGCATCCGTCGACCA 300
QY 301 GGGACACGACTGGACATTTCAA 321
DB 301 GGGACCAAGCTGGAGATCAA 321

RESULT 9 BD075293 321 bp DNA linear PAT 27-AUG-2002
LOCUS BD075293
DEFINITION Novel method for the production of anti-human antigen receptors and uses thereof.

ACCESSION BD075293
VERSION BD075293.1 GI:22620896
KEYWORDS JP 2001519824-A/22.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Kufner, P. and Raum, T.
TITLE 1 (bases 1 to 321)
JOURNAL Novel method for the production of anti-human antigen receptors and uses thereof.

COMMENT Patent: JP 2001519824-A 22 23-OCT-2001;
MICROMET AG
OS Homo sapiens (human)
PN JP 2001519824-A/22

PD 23-OCT-2001
PF 14-APR-1998 JP 1998543494
PR 14-APR-1997 EP 97106109.8
PI PETER KUFNER, TOBIAS RAUM
PC C07K16/00, C07K16/30, A61K39/395
CC Novel method for the production of anti-human antigen receptors and uses thereof

FEATURES
source 1..321
FT CDS Location/Qualifiers
1..321
Location/Qualifiers
1..321

FEATURES
source 1..321
FT CDS Location/Qualifiers
1..321
Location/Qualifiers
1..321

Query Match

81.1%; Score 260.2; DB 6; Length 321;

Best Local Similarity 88.2%; Pred. No. 1e-76;
Matches 283; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTCTGATCTGTAGAGACAGAGTACC 60
DB 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTCTGATCTGTAGAGACAGAGTACC 60
QY 61 ATACTTTGCCGGCAAGTCAAGACATTAGACGCTATTAAATTGGTATACGCAAAACCA 120
DB 61 ATACTTTGCCGGCAAGTCAAGACATTAGACGCTATTAAATTGGTATACGCAAAACCA 120
QY 121 GGACAGCTCTTAAGCTGCTCATTTTCTGGGCACTTACCGGGAAATCCGGGGTCCCTGAC 180
DB 121 GGACAGCTCTTAAGCTGCTCATTTTCTGGGCACTTACCGGGAAATCCGGGGTCCCTGAC 180
QY 181 CGATTGAGCGGCGAGTGAATCTGGGCAAAATTACACTCTACATCAGACAGCTGACGCT 240
DB 181 CGATTGAGCGGCGAGTGAATCTGGGCAAAATTACACTCTACATCAGACAGCTGACGCT 240
QY 241 GAAGATTTTGTCTACTTACTTTTGTCAACAGTCTGACAGATTGCGCATCCGTCGACCA 300
DB 241 GAAGATTTTGTCTACTTACTTTTGTCAACAGTCTGACAGATTGCGCATCCGTCGACCA 300
QY 301 GGGACACGACTGGACATTTCAA 321
DB 301 GGGACCAAGCTGGAGATCAA 321

RESULT 10 BD139668 321 bp DNA linear PAT 18-SEP-2002
LOCUS BD139668
DEFINITION A novel method of identifying binding site domains that retain the capacity of binding to an epitope.

ACCESSION BD139668
VERSION BD139668.1 GI:23234613
KEYWORDS JP 2002508924-A/53.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Kufner, P., Raum, T., Borschert, K., Zetel, F. and Lutterbuese, R.
TITLE 1 (bases 1 to 321)
JOURNAL A novel method of identifying binding site domains that retain the capacity of binding to an epitope.

COMMENT Patent: JP 2002508924-A 53 26-MAR-2002;
PETER KUFNER
OS Homo sapiens (human)
PN JP 2002508924-A/53

PD 26-MAR-2002 JP 2000521184
PF 16-NOV-1998 JP 2000521184
PR 17-NOV-1997 EP 97120096.9
PI PETER KUFNER, TOBIAS RAUM, KATRIN BORSCHERT, FLORIAN ZETTEL, RALF LUTTERBUESE
PC C12N15/09, A61K38/00, A61K38/22, A61K38/43, A61K39/395, C07K14/705, PC C07K16/30,
PC C12N1/21, C12N5/10, C12P21/02, C12P21/08, G01N33/566, C12N15/00, PC A61K37/02,
PC A61K37/24, A61K37/48, C12N5/00

CC A novel method of identifying binding site domains that retain the capacity of binding to an epitope

FEATURES
source 1..321
FT Key Location/Qualifiers
1..321
Location/Qualifiers
1..321

FEATURES
source 1..321
FT Key Location/Qualifiers
1..321
Location/Qualifiers
1..321

Query Match

81.1%; Score 260.2; DB 6; Length 321;

Best Local Similarity 88.2%; Pred. No. 1e-76;
Matches 283; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1 GAGCTCAGATGACCCAGTCTCATCTCCCTGTGATCTGTAGAGACAGAGTACC 60
Db 1 GAGCTCAGATGACCCAGTCTCATCTCCCTGTGATCTGTAGAGACAGAGTACC 60
QY 61 ATCACTTGGCGGAGAGTCAAGACATTAAGCATTTAAATTTGGTATCAGAGAAACA 120
Db 61 ATCACTTGGCGGAGAGTCAAGACATTAAGCATTTAAATTTGGTATCAGAGAAACA 120
QY 121 GGACAGCCTCTAAGCTGCTCATTTTACTGGGACATCAACCAGGAATCCGGGCTCCTGAC 180
Db 121 GGACAGCCTCTAAGCTGCTCATTTTACTGGGACATCAACCAGGAATCCGGGCTCCTGAC 180
QY 181 CGATTGAGCGGAGAGTGAATCTGGACAAATTACCTTCACATCCAGAGCTGACGCT 240
Db 181 CGATTGAGCGGAGAGTGAATCTGGACAAATTACCTTCACATCCAGAGCTGACAACT 240
QY 241 GAAGATTTTGTCTTACTTTTGTCAACAGTCTGACAGTTTGGCCATCCTGGCCAA 300
Db 241 GAAGATTTTGTCAACTTACTACTGTGACAGAGTTTACAGATCCGTTACTTTGGCCAG 300
QY 301 GGGACAGACTGGACATTCNA 321
Db 301 GGGACAGACTGGAGATCAAA 321

RESULT 11
BD187178 324 bp DNA linear PAT 17-JUN-2003
LOCUS Human-typed antibody against blood coagulation factor VIII.
DEFINITION BD187178.1 GI:31879467
ACCESSION WO 02101040-A/7.
VERSION
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 324)
AUTHORS Nakashima, T. and Yuguchi, M.
TITLE Human-typed antibody against blood coagulation factor VIII
JOURNAL Patent: WO 02101040-A 7 19-DEC-2002;
JURIDICAL FOUNDATION THE CHEMO SERO THERAPEUTIC RESEARCH INSTITUTE,
TOSHIHIRO NAKASHIMA, MASATO YUGUCHI
OS Homo sapiens (human)
PN WO 02101040-A/7
PD 19-DEC-2002
PF 11-JUN-2002 WO 2002JP005783
PI 12-JUN-2001 JP 01P 177640
PT TOSHIHIRO NAKASHIMA, MASATO YUGUCHI
PC C12N15/09, C07K16/14, C07K7/06, C07K7/08, C12P21/08, G01N33/53 CC
Human-typed antibody against blood coagulation factor VIII FH Key
Location/Qualifiers
FT source 1..324
/organism='Homo sapiens (human)'.
Location/Qualifiers
1..324
/mol_type='genomic DNA'
/db_xref='taxon:9606'

ORIGIN
Query Match 76.6%; Score 245.8; DB 6; Length 324;
Best Local Similarity 85.4%; Pred. No. 7.9e-72;
Matches 274; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 GAGCTCAGATGACCCAGTCTCATCTCCCTGTGATCTGTAGAGACAGAGTACC 60
Db 1 GAGCTCAGATGACCCAGTCTCATCTCCCTGTGATCTGTAGAGACAGAGTACC 60
QY 61 ATCACTTGGCGGAGAGTCAAGACATTAAGCATTTAAATTTGGTATCAGAGAAACA 120
Db 61 ATCACTTGGCGGAGAGTCAAGACATTAAGCATTTAAATTTGGTATCAGAGAAACA 120

Db 61 ATCACTTGGCGGAGAGTCAAGACATTAAGCATTTAAATTTGGTATCAGAGAAACA 120
QY 121 GGACAGCCTCTAAGCTGCTCATTTTACTGGGACATCAACCAGGAATCCGGGCTCCTGAC 180
Db 121 GGACAGCCTCTAAGCTGCTCATTTTACTGGGACATCAACCAGGAATCCGGGCTCCTGAC 180
QY 181 CGATTGAGCGGAGAGTGAATCTGGACAAATTACCTTCACATCCAGAGCTGACGCT 240
Db 181 AGTTTCAAGTGGAGAGTGAATCTGGACAAATTACCTTCACATCCAGAGCTGACAACT 240
QY 241 GAAGATTTTGTCTTACTTTTGTCAACAGTCTGACAGTTTGGCCATCCTGGCCAA 300
Db 241 GAAGATTTTGTCAACTTACTACTGTGACAGAGTTTACAGATCCGTTACTTTGGCCAA 300
QY 301 GGGACAGACTGGACATTCNA 321
Db 301 GGGACAGACTGGAGATTA 321

RESULT 12
BD187179 324 bp DNA linear PAT 17-JUN-2003
LOCUS Human-typed antibody against blood coagulation factor VIII.
DEFINITION BD187179.1 GI:31879468
ACCESSION WO 02101040-A/8.
VERSION
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 324)
AUTHORS Nakashima, T. and Yuguchi, M.
TITLE Human-typed antibody against blood coagulation factor VIII
JOURNAL Patent: WO 02101040-A 8 19-DEC-2002;
JURIDICAL FOUNDATION THE CHEMO SERO THERAPEUTIC RESEARCH INSTITUTE,
TOSHIHIRO NAKASHIMA, MASATO YUGUCHI
OS Homo sapiens (human)
PN WO 02101040-A/8
PD 19-DEC-2002 WO 2002JP005783
PF 11-JUN-2002 JP 01P 177640
PI TOSHIHIRO NAKASHIMA, MASATO YUGUCHI
PC C12N15/09, C07K16/14, C07K7/06, C07K7/08, C12P21/08, G01N33/53 CC
Human-typed antibody against blood coagulation factor VIII FH Key
Location/Qualifiers
FT source 1..324
/organism='Homo sapiens (human)'.
Location/Qualifiers
1..324
/mol_type='genomic DNA'
/db_xref='taxon:9606'

ORIGIN
Query Match 76.6%; Score 245.8; DB 6; Length 324;
Best Local Similarity 85.4%; Pred. No. 7.9e-72;
Matches 274; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 GAGCTCAGATGACCCAGTCTCATCTCCCTGTGATCTGTAGAGACAGAGTACC 60
Db 1 GAGCTCAGATGACCCAGTCTCATCTCCCTGTGATCTGTAGAGACAGAGTACC 60
QY 61 ATCACTTGGCGGAGAGTCAAGACATTAAGCATTTAAATTTGGTATCAGAGAAACA 120
Db 61 ATCACTTGGCGGAGAGTCAAGACATTAAGCATTTAAATTTGGTATCAGAGAAACA 120
QY 121 GGACAGCCTCTAAGCTGCTCATTTTACTGGGACATCAACCAGGAATCCGGGCTCCTGAC 180
Db 121 GGACAGCCTCTAAGCTGCTCATTTTACTGGGACATCAACCAGGAATCCGGGCTCCTGAC 180
QY 181 CGATTGAGCGGAGAGTGAATCTGGACAAATTACCTTCACATCCAGAGCTGACGCT 240
Db 181 AGTTTCAAGTGGAGAGTGAATCTGGACAAATTACCTTCACATCCAGAGCTGACAACT 240

Db 241 GAGATTTTGTCTACTTTTGTCAAGCTGTGACAGTTTGGCGATCACTTGGCCAA 300
|||||
241 GAGATTTTGTCAACTTACTGTCTCAACAGATTACAGTCCCGATCACTTGGCCAA 300
OY 301 GGGACACGACTGGACATTCAA 321
|||||
Db 301 GGGACACGACTGGACATTCAA 321
|||||

RESULT 13
AB006842 339 bp mRNA linear PRI 09-SEP-1997
LOCUS Homo sapiens mRNA for HRV Fab N6-VL, partial cds.
DEFINITION AB006842.1 GI:2385484
ACCESSION AB006842.1 GI:2385484
VERSION
KEYWORDS HRV Fab N6-VL.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 339)
AUTHORS Itoh, K. and Suzuki, T.
TITLE Human anti-rotavirus Fabs
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 339)
AUTHORS Itoh, K.
TITLE Direct Submission
JOURNAL Submitted (26-AUG-1997) Kunihiko Itoh, Akita University Hospital,
Pharmaceutical Science, Hondo 1-1-1, Akita, Akita 010, Japan
(E-mail: itohk@hos.akita-u.ac.jp, Tel: +81-188-34-1111,
Fax: +81-188-36-2628)

FEATURES
source Location/Qualifiers
1..339
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cistype="PBL"
1..3339
/codon_start=1
/product="HRV Fab N6-VL"
/protein_id="BAA2181.1"
/db_xref="GI:2385485"
/translation="MAELVMTOSPPSLASVGDRTVFTCRASQSSISYINWYQKRG
AKLTIYASSLQSGVPSRFSGSGSTDTLTLSLQPDPAFTYQGSYSTPTFGQ
GRLEIKRTVA"

ORIGIN
Query Match 76.1%; Score 244.2; DB 9; Length 339;
Best Local Similarity 85.0%; Pred. No. 2.8e-71;
Matches 273; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

OY 1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTGTCATCTGTAGAGACAGAGTCACC 60
|||||
Db 7 GAGCTGTATGACCCAGTCTCCATCCTCCCTGTGTCATCTGTAGAGACAGAGTCACC 66
|||||

OY 61 ATCACTTCCCGGCAAGTCAAGACATTAAGCACTATTAAATGGTATACAGAAACCA 120
|||||
Db 67 TTCACTTCCCGGCAAGTCAAGACATTAAGCACTATTAAATGGTATACAGAAACCA 126
|||||

OY 121 GGAAGCCCTCTAAGCTGCTCATTTACTGGGCACTACCCGGGAATCCGGGGTCCCTGAC 180
|||||
Db 127 GGAAGCCCTCTAAGCTGCTCATTTACTGGGCACTACCCGGGAATCCGGGGTCCCTGAC 186
|||||

OY 181 CGATTCAAGGGAGATGATCTGGGCAAAATTAACACTCTACCATCAGACGCTGACCT 240
|||||
Db 187 AGGTCAGAGGAGATGATCTGGGCAAAATTAACACTCTACCATCAGAGTCTGCAACT 246
|||||

OY 241 GAAAGTTTGTCTACTTTTGTCAACAGTCTGACAGTTTGGCGATCACTTGGCCAA 300
|||||
Db 247 GAAAGTTTGTCAACTTACTGTCTCAACAGATTACAGTATCCGATCACTTGGCCAA 306
|||||

OY 301 GGGACACGACTGGACATTCAA 321
|||||

Db 307 GGGACACGACTGGACATTCAA 327
|||||

RESULT 14
BD097614 342 bp DNA linear PAT 27-AUG-2002
LOCUS BD097614
DEFINITION Antibody library.
ACCESSION BD097614
VERSION BD097614.1 GI:22643188
KEYWORDS WO 0162907-A/69.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 342)
AUTHORS Kurosawa, Y., Akahori, Y., Iba, Y., Morino, K., Shinohara, M.,
Takahashi, M., Okuno, Y. and Shiraki, K.
TITLE Antibody library
JOURNAL Patent: WO 0162907-A 69 30-AUG-2001;
MEDICAL & BIOLOGICAL LABORATORIES CO LTD, YOSHIKAZU KUROSAWA,
YASUSHI AKAHORI, YOSHITAKA IBA, KAZUHIKO MORINO, MIDORI SHINOHARA,
MOTOHIDE TAKAHASHI, YOSHINOBU OKUNO, KIMIYASU SHIRAKI
OS Homo sapiens (human)
PN WO 0162907-A/69
PD 30-AUG-2001
PF 22-FEB-2001 WO 2001JP001298
PR 22-FEB-2001 JP 00P 50543
PI YOSHIKAZU KUROSAWA, YASUSHI AKAHORI, YOSHITAKA IBA, KAZUHIKO PI
MORINO.
PI MIDORI SHINOHARA, MOTOHIDE TAKAHASHI, YOSHINOBU OKUNO, KIMIYASU
PI SHIRAKI
PC C12N15/09, C07K16/00//C12P21/08
CC Antibody library
FH Key
FT source Location/Qualifiers
1..342
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 76.1%; Score 244.2; DB 6; Length 342;
Best Local Similarity 85.0%; Pred. No. 2.8e-71;
Matches 273; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

OY 1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTGTCATCTGTAGAGACAGAGTCACC 60
|||||
Db 1 GAGCTGTATGACCCAGTCTCCATCCTCCCTGTGTCATCTGTAGAGACAGAGTCACC 66
|||||

OY 61 ATCACTTCCCGGCAAGTCAAGACATTAAGCACTATTAAATGGTATACAGAAACCA 120
|||||
Db 61 ATCACTTCCCGGCAAGTCAAGACATTAAGCACTATTAAATGGTATACAGAAACCA 120
|||||

OY 121 GGAAGCCCTCTAAGCTGCTCATTTACTGGGCACTACCCGGGAATCCGGGGTCCCTGAC 180
|||||
Db 121 GGAAGCCCTCTAAGCTGCTCATTTACTGGGCACTACCCGGGAATCCGGGGTCCCTGAC 180
|||||

OY 181 CGATTCAAGGGAGATGATCTGGGCAAAATTAACACTCTACCATCAGACGCTGACCT 240
|||||
Db 181 AGGTCAGAGGAGATGATCTGGGCAAAATTAACACTCTACCATCAGAGTCTGCAACT 240
|||||

OY 241 GAAAGTTTGTCTACTTTTGTCAACAGTCTGACAGTTTGGCGATCACTTGGCCAA 300
|||||
Db 241 GAAAGTTTGTCAACTTACTGTCTCAACAGATTACAGTATCCGATCACTTGGCCAA 300
|||||

OY 301 GGGACACGACTGGACATTCAA 321
|||||
Db 301 GGGACACGACTGGACATTCAA 321
|||||

RESULT 15
BD097618
LOCUS BD097618 321 bp DNA linear PAT 27-AUG-2002
DEFINITION Antibody library.
ACCESSION BD097618
VERSION BD097618.1 GI:22643192
KEYWORDS WO 0162907-A/73.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 321)
Kurosawa, Y., Akahori, Y., Iba, Y., Morino, K., Shinohara, M.,
Takahashi, M., Okuno, Y. and Shiraki, K.
TITLE Antibody library
JOURNAL Patent: WO 0162907-A 73 30-AUG-2001;
MEDICAL & BIOLOGICAL LABORATORIES CO LTD YOSHIKAZU KUROSAWA,
YASUSHI AKAHORI, YOSHITAKA IBA, KAZUHIKO MORINO, MIDORI SHINOHARA,
MOTOHIDE TAKAHASHI, YOSHINOBU OKUNO, KIMIYASU SHIRAKI
COMMENT OS Homo sapiens (human)
PN WO 0162907-A/73
PD 30-AUG-2001
PF 22-FEB-2001 WO 2001JP001298
PR 22-FEB-2000 JP 00P 50543
PI YOSHIKAZU KUROSAWA, YASUSHI AKAHORI, YOSHITAKA IBA, KAZUHIKO PI
MORINO,
PI MIDORI SHINOHARA, MOTOHIDE TAKAHASHI, YOSHINOBU OKUNO, KIMIYASU
SHIRAKI
PC C12N15/09, C07K16/00//C12P21/08
CC Antibody library
FH Key Location/Qualifiers
FT source 1..321
location/Qualifiers
1..321
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 75.6%; Score 242.6; DB 6; Length 321;
Best Local Similarity 84.7%; Pred. No. 9,7e-71;
Matches 272; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 1 GAGCTCCAGATGAGCCAGTCTCCATCTCTCTGTCATCTGTAGAGACAGAGTCACC 60
DB 1 GACATCGTATGATCCAGTCTCCATCTCTCTGTCATCTGTAGAGACAGAGTCACC 60
QY 61 ATCTCTGCGGGGAGAACTCAGAGATAGAGCTATTAAATGGTATCAGAGAAACCA 120
DB 61 ATCACTTGGCGGGGAGAACTCAGAGATAGAGCTATTAAATGGTATCAGAGAAACCA 120
QY 121 GGACAGCCTCTCTAGTCTCATTTACTGTGGGCACTACCCGGGAAATCCGGGGTCCCTGAC 180
DB 121 GGGAAGCCCTTAGTCTCTGATCTATGCTGCATCCAGTTTGCAAGTGGGATCCCATCA 180
QY 181 CGATTACAGCGGAGATGATCTGGGACAAATTACCTCTCACCATCAGCAGCTGGAGCTT 240
DB 181 AGTTTCAGTGGAGTGTGATCTGGGACAGATTTCCTCACCATCAGCAGCTGGAGCTT 240
QY 241 GAAGATTTTGCTACTTCTTTGTCACAAGTCTGACAGTTTGGCGATCACCTTGGGCCAA 300
DB 241 GAAGATTTTGCTACTTCTTTGTCACAAGTCTGACAGTTTGGCGATCACCTTGGGCCAA 300
QY 301 GGACACGACTGACATTCAA 321
DB 301 GGACACGACTGACATTCAA 321

Search completed: December 7, 2004, 08:53:05
Job time: 1816.78 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 22:52:33 ; Search time 271.757 Seconds
(without alignments)
6200.629 Million cell updates/sec

Title: US-09-403-107-147

Perfect score: 321

Sequence: 1 ggagccacagatgaccacagtc.....ggacacgactggacattcaa 321

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_23sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	321	100.0	321	2	AAV68539
2	321	100.0	1630	3	AAZ50588
3	321	100.0	1630	3	AAZ50587
4	260.2	81.1	321	2	AAV68536
5	260.2	81.1	321	2	AAV77237
6	249	77.6	321	11	AAO51603
7	245.8	76.6	324	10	AAI52122
8	244.2	76.1	342	4	AAH47727
9	242.6	75.6	321	4	AAH47731
10	240.8	75.0	321	5	AAH68651
11	240.8	75.0	321	9	ACD45315
12	240.2	74.8	321	12	ADO36505
13	240.2	74.3	327	10	ADO36497
14	238.6	74.3	327	10	ADP89879
15	237.8	74.1	321	12	ADP22249
16	237.8	74.1	324	4	AA503434
17	236.2	73.6	321	11	AD051602
18	236.2	73.6	321	12	ADP22235
19	236.2	73.6	321	12	ADP22253
20	236.2	73.6	458	12	ADK52349
21	235	73.2	1106	6	ABQ54241

22	234.4	73.0	936	3	AAZ7390	AAZ7390 Human IGF
23	223	72.6	321	12	ADP22243	ADP22243 Human ant
24	232.8	72.5	917	3	AAZ7381	AAZ7381 Human IGF
25	231.4	72.1	333	5	AAH74684	AAH74684 Nucleotid
26	231.4	72.1	333	10	ABT34320	ABT34320 Hepatitis
27	231.4	72.1	720	2	AAK36070	AAK36070 DNA encod
28	231.4	72.1	720	10	ABT76706	ABT76706 Human ser
29	231.4	72.1	720	12	ADL92368	ADL92368 Human pha
30	231.4	72.1	900	5	AAH74688	AAH74688 Nucleotid
31	231.4	72.1	900	10	ABT34324	ABT34324 Hepatitis
32	229.8	71.6	321	9	AAZ57375	AAZ57375 Human SFI
33	229.8	71.6	324	10	AAI52120	AAI52120 Human ant
34	229.8	71.6	396	2	AAI75423	AAI75423 Human ant
35	229.8	71.6	684	4	AAH30052	AAH30052 TRO005 Ka
36	229.8	71.6	720	10	ABT34315	ABT34315 Hepatitis
37	229.8	71.6	729	3	AAI1630	AAI1630 Human imm
38	229.8	71.6	729	6	ABL46009	ABL46009 Humanised
39	228.2	71.1	321	11	AD051601	AD051601 Human TAG
40	228.2	71.1	324	4	AAI29073	AAI29073 Human HIV
41	228.2	71.1	324	4	AAI29073	AAI29073 Human HIV
42	228.2	71.1	324	12	ADL92385	ADL92385 Anti-HSA
43	228.2	71.1	714	3	AAI46899	AAI46899 DNA encod
44	228.2	71.1	714	10	AAI54350	AAI54350 Human 11
45	228.2	71.1	819	10	AAI59178	AAI59178 Human Ig

ALIGNMENTS

RESULT 1	AAV68539	AAV68539 standard; DNA; 321 BP.
AC	AAV68539;	
AC	AAV68539;	
DT	16-FEB-1999	(first entry)
DE	Nucleotide sequence of human kappa 5.1 light chain variable region.	
XX	Human; kappa 5.1 light chain variable region; receptor; antigen; tumour;	
KW	auto-immune disease; graft rejection; allergy; inflammatory disease;	
KW	endocrine disease; degenerative disease; ss.	
OS	Homo sapiens.	
XX	Key	
XX	Location/Qualifiers	
FT	1..321	
FT	/*tag= a	
XX	/product= "human kappa 5.1 light chain variable region"	
XX	WO9846645-A2.	
XX	22-OCT-1998.	
PD	14-APR-1998; 98WO-EP002180.	
XX	14-APR-1997; 97EP-00106109.	
PR	(KUFE/) KUFER P.	
PA	(RAUM/) RAUM T.	
XX	Kufer P, Raum T;	
XX	WPI; 1998-594564/50.	
DR	P-PDB; AAV68539.	
XX	Production of anti-human antigen receptors - by selecting a combination	
PT	of functionally rearranged VH and VL immunoglobulin chains expressed from	
PT	a recombinant vector.	
XX	Claim 9; Fig 9; 84p; English.	
CC	This is the nucleotide sequence of the human kappa light chain variable	

CC region, used in the method of the invention, for providing receptors that
CC can be used for targeting antigens in humans without being immunogenic
CC themselves. Such receptors can be used for treating diseases such as
CC tumours or auto-immune diseases, graft rejection after transplantation,
CC infectious diseases by targeting cellular receptors as well as allergic,
CC inflammatory, endocrine and degenerative diseases by targeting key
CC molecules involved in the pathological process

XX Sequence 321 BP; 81 A; 93 C; 72 G; 75 T; 0 U; 0 Other;

Query Match 100.0%; Score 321; DB 2; Length 321;
Best Local Similarity 100.0%; Pred. No. 1.3e-93;

Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTGTGATCTGTAGAGACAGAGTACCC 60
    |||
DB 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTGTGATCTGTAGAGACAGAGTACCC 60
QY 61 ATCACTGCGGGCAGTCAAGACATTAAGAGCTATTAAATGGTATCAGAGAAACCA 120
    |||
DB 61 ATCACTGCGGGCAGTCAAGACATTAAGAGCTATTAAATGGTATCAGAGAAACCA 120
QY 121 GGACAGCTCTCTAAGCTGTCTATTACTGTGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
    |||
DB 121 GGACAGCTCTCTAAGCTGTCTATTACTGTGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
QY 181 CGATTGAGGGGCGAGTGAATGTGGGCAAAATTACATCTCACCATCGACGCTGACGCT 240
    |||
DB 181 CGATTGAGGGGCGAGTGAATGTGGGCAAAATTACATCTCACCATCGACGCTGACGCT 240
QY 241 GAAGATTTTGTCTACTTCTTTGTCAACAGTGTGACAGTTGGCCGATCCTTGGCCAA 300
    |||
DB 241 GAAGATTTTGTCTACTTCTTTGTCAACAGTGTGACAGTTGGCCGATCCTTGGCCAA 300
QY 301 GGGACACGACTGGACATTCA 321
    |||
DB 301 GGGACACGACTGGACATTCA 321
```

RESULT 2

AAZ50588 ID AAZ50588 standard; DNA; 1630 BP.

XX AC AAZ50588;

XX DT 23-MAY-2000 (first entry)

XX DE HD70scFv-CK-interleukin 2 encoding DNA.

KW HD70: single-chain variable fragment; scFv; 17-1A antigen; human; EPCAM;
KW epithelial cell adhesion molecule; inflammatory cytokine; IL-2;
KW interleukin-2; Ck-domain; kappa light chain constant domain;
KW heteromultibody; multifunctional compound; immunoglobulin; cytostatic;
KW immunostimulatory; antileukemia; diagnosis; prevention;
KW antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;
KW leukemia; solid tumour; carcinoma; melanoma; sarcoma; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 39..1613

XX FT FT /*tag= a

XX FT FT /product= "HD70scFv-CK-IL-2 chain"

XX FT FT 96..842

XX FT FT /*tag= b

XX FT FT /label= HD70_scFv

XX PN WO200006605-A2.

XX PD 10-FEB-2000.

XX PF 28-JUL-1999; 99WO-EP005416.

PR 28-JUL-1998; 98EP-00114082.

XX (MIR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.

XX Kufer P, Dreier T, Baeuerle PA, Borsche K, Zetl F;

XX WPI: 2000-195265/17.

XX P-PSDB; AAY44995.

PT New multifunctional compounds useful for preventing and/or treating
PT malignant cell growth and for detection and diagnosis.

PS Claim 8; Fig 55B; 166pp; English.

CC The patent discloses heteromultibodies which are multifunctional compounds
CC producible in a mammalian host cell as a secretable and fully functional
CC heterodimer of two polypeptide chains, where one of the polypeptide
CC chains comprises, a CH1-domain (constant domain of an immunoglobulin
CC heavy chain) and the other chain comprises CL-domain (constant domain of
CC an immunoglobulin light chain). The polypeptide chains further comprise,
CC fused to the constant domains at least two (polypeptides having
CC different receptor or ligand functions, where further at least two of the
CC different (poly)peptides lack an intrinsic affinity for one another and
CC are linked via the constant domains. The heteromultibodies have
CC cytostatic, immunostimulatory, antileukemia and antiproliferative
CC activities. These compounds can be used for diagnosing, preventing and
CC treating malignant cell growth related to malignancies of hematopoietic
CC cells e.g. lymphomas and leukemias, or to solid tumours e.g. carcinomas,
CC melanomas and sarcomas. The present sequence is a DNA encoding right
CC chain of a heteromultibody comprising HD70 single-chain Fv (scFv) fragment
CC N-terminally linked to human Ck domain (constant domain of immunoglobulin
CC -kappa light chain) which bears at its C-terminus the human inflammatory
CC cytokine interleukin-2 (IL-2). HD70 scFv specifically recognises the
CC human epithelial cell adhesion molecule (EPCAM) also called 17-1A antigen

XX SQ Sequence 1630 BP; 445 A; 410 C; 408 G; 367 T; 0 U; 0 Other;

Query Match 100.0%; Score 321; DB 3; Length 1630;

Best Local Similarity 100.0%; Pred. No. 2.5e-93;

Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTGTGATCTGTAGAGACAGATCAC 60
    |||
DB 96 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTGTGATCTGTAGAGACAGATCAC 155
QY 61 ATCACTGCGGGCAGTGAATGTGGGCAAAATTACATCTCACCATCGACGCTGACGCT 120
    |||
DB 156 ATCACTGCGGGCAGTGAATGTGGGCAAAATTACATCTCACCATCGACGCTGACGCT 215
QY 121 GGACAGCTCTCTAAGCTGTCTATTACTGTGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
    |||
DB 216 GGACAGCTCTCTAAGCTGTCTATTACTGTGGCATCTACCCGGGAATCCGGGGTCCCTGAC 275
QY 181 CGATTGAGGGGCGAGTGAATGTGGGCAAAATTACATCTCACCATCGACGCTGACGCT 240
    |||
DB 276 CGATTGAGGGGCGAGTGAATGTGGGCAAAATTACATCTCACCATCGACGCTGACGCT 335
QY 241 GAAGATTTTGTCTACTTCTTTGTCAACAGTGTGACAGTTGGCCGATCCTTGGCCAA 300
    |||
DB 336 GAAGATTTTGTCTACTTCTTTGTCAACAGTGTGACAGTTGGCCGATCCTTGGCCAA 395
QY 301 GGGACACGACTGGACATTCA 321
    |||
DB 396 GGGACACGACTGGACATTCA 416
```

RESULT 3

AAZ50587 ID AAZ50587 standard; DNA; 1630 BP.

XX AC AAZ50587;

XX DT 23-MAY-2000 (first entry)

```

XX DE HD70scFv-CHI-GM-CSF chain encoding DNA.
XX XX
XX HD70, single-chain variable fragment; scFv; 17-1A antigen; human; EPCAM;
XX epithelial cell adhesion molecule; inflammatory cytokine; GM-CSF;
XX granulocyte/macrophage colony stimulating factor; heteromultibody;
XX CHI-domain; multifunctional compound; heavy chain constant domain;
XX immunoglobulin; cytostatic; immunostimulatory; anti-leukemia; diagnosis;
XX antiproliferative; prevention; treatment; malignant; haematopoietic cell;
XX lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma; ds.
OS Homo sapiens.
XX XX
XX Key Location/Qualifiers
XX FT CDS 39..1610
XX FT /*tag= a
XX FT /product= "HD70scFv-CHI-GM-CSF chain"
XX FT misc_feature 96..842
XX FT /*tag= b
XX FT /label= HD70_scFv
XX XX
XX WO200006605-A2.
XX PN
XX PD 10-FEB-2000.
XX XX
XX PF 28-JUL-1999; 99WO-EP005416.
XX XX
XX PR 28-JUL-1998; 98BP-00114082.
XX XX
XX (MIGR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
XX PA Kufer P, Dreier T, Baueerle PA, Borschert K, Zetcl F;
XX PI WPI; 2000-195265/17.
XX DR P-PSDB; AAY44994.
XX XX
XX New multifunctional compounds useful for preventing and/or treating
XX malignant cell growth and for detection and diagnosis.
XX PT
XX PS Claim 8; Fig 55A; 166pp; English.
XX XX
XX The patent discloses heteromultibodies which are multifunctional compounds
XX producible in a mammalian host cell as a secretable and fully functional
XX heterodimer of two polypeptide chains, where one of the polypeptide
XX chains comprises a CHI-domain (constant domain of an immunoglobulin
XX heavy chain) and the other chain comprises CL-domain (constant domain of
XX an immunoglobulin light chain). The polypeptide chains further comprise,
XX fused to the constant domains at least two (poly)peptides having
XX CC different receptor or ligand functions, where further at least two of the
XX CC different (poly)peptides lack an intrinsic affinity for one another and
XX CC are linked via the constant domains. The heteromultibodies have
XX CC cytostatic, immunostimulatory, anti-leukemia and antiproliferative
XX CC activities. These compounds can be used for diagnosing, preventing and
XX CC treating malignant cell growth related to malignancies of haematopoietic
XX CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
XX CC melanomas and sarcomas. The present sequence is a DNA encoding left chain
XX CC of a heteromultibody comprising HD70 single-chain Fv (scFv) fragment N-
XX CC terminally linked to human CHI domain which bears at its C-terminus the
XX CC human inflammatory cytokine granulocyte/macrophage colony stimulating
XX CC factor (GM-CSF), plus a hexahistidine sequence for ease of purification.
XX CC HD70 scFv specifically recognises the human epithelial cell adhesion
XX CC molecule (EPCAM) also called 17-1A antigen
XX XX
XX Sequence 1630 BP; 376 A; 484 C; 437 G; 333 T; 0 U; 0 Other;
SQ

```

```

Query Match 100.0%; Score 321; DB 3; Length 1630;
Best Local Similarity 100.0%; Pred. No. 2.5e-93;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCTGTCATCTGTAGAGACAGAGTCCACC 60
DB 96 GAGCTCCAGATGACCCAGTCTCCATCTCTGTCATCTGTAGAGACAGAGTCCACC 155

```

```

QY 61 ATCACTTGGCCGGGCAAGTCAGACATTTAGACGCTATTTAAATTGTAACAGAGAAACCA 120
DB 156 ATCACTTGGCCGGGCAAGTCAGACATTTAGACGCTATTTAAATTGTAACAGAGAAACCA 215
QY 121 GGACAGCCTCTTAAGCTGCTCATTTTACTGGGACTTACCGGGAATCCGGGGTCCCTGAC 180
DB 216 GGACAGCCTCTTAAGCTGCTCATTTTACTGGGACTTACCGGGAATCCGGGGTCCCTGAC 275
QY 181 CGATTGAGCGGCGAGTGAATCTGGGCAAAATTACCTTCACATCAGACAGCCTGACGCT 240
DB 276 CGATTGAGCGGCGAGTGAATCTGGGCAAAATTACCTTCACATCAGACAGCCTGACGCT 335
QY 241 GAAATTTTGTCTTACTTACTTTTGTCAACAGTCTGAAGTTTGGCCATTCACCTTGGCCCA 300
DB 336 GAAATTTTGTCTTACTTACTTTTGTCAACAGTCTGAAGTTTGGCCATTCACCTTGGCCCA 395
QY 301 GGGACAGACTGACATTCGA 321
DB 396 GGGACAGACTGACATTCGA 416

RESULT 4
AAV68536
ID AAV68536 standard; DNA; 321 BP.
XX AC
XX AAV68536;
XX DT 16-FEB-1999 (first entry)
XX XX
XX Nucleotide sequence of human kappa 8 light chain variable region.
XX DE
XX Human; kappa 8 light chain variable region; receptor; antigen; tumour;
XX KM auto-immune disease; graft rejection; allergy; inflammatory disease;
XX KM endocrine disease; degenerative disease; ss.
XX OS Homo sapiens.
XX XX
XX Key Location/Qualifiers
XX FT CDS 1..321
XX FT /*tag= a
XX FT /product= "human kappa 8 light chain variable region"
XX XX
XX WO9846645-A2.
XX PN
XX PD 22-OCT-1998.
XX XX
XX PF 14-APR-1998; 98WO-EP002180.
XX XX
XX PR 14-APR-1997; 97BP-00106109.
XX XX
XX (KUFE/) KUFER P.
XX PA (RAUM/) RAUM T.
XX XX
XX Kufer P, Raum T;
XX PI WPI; 1998-594564/50.
XX DR P-PSDB; AAW60814.
XX XX
XX Production of anti-human antigen receptors - by selecting a combination
XX PT of functionally rearranged VH and VL immunoglobulin chains expressed from
XX PT a recombinant vector.
XX XX
XX Claim 9; Fig 6; 84pp; English.
XX PS
XX XX
XX This is the nucleotide sequence of the human kappa 8 light chain variable
XX CC region, used in the method of the invention, for providing receptors that
XX CC can be used for targeting antigens in humans without being immunogenic
XX CC themselves. Such receptors can be used for treating diseases such as
XX CC tumours or auto-immune diseases, graft rejection after transplantation,
XX CC infectious diseases by targeting cellular receptors as well as allergic,
XX CC inflammatory, endocrine and degenerative diseases by targeting key
XX CC molecules involved in the pathological process

```

SQ Sequence 321 BP; 81 A; 91 C; 75 G; 74 T; 0 U; 0 Other;
 Query Match 81.1%; Score 260.2; DB 2; Length 321;
 Best Local Similarity 88.2%; Pred. No. 6.6e-74;
 Matches 283; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGATCTCCCTCTGTCATCTGTAGAGACAGATCACC 60
 DB 1 GAGCTCCAGATGACCCAGATCTCCCTCTGTCATCTGTAGAGACAGATCACC 60
 QY 61 ATCACTTGGCCGGGCAAGTCAAGATAGAGATTAATTTGATCAGAGAAACCA 120
 DB 61 ATCACTTGGCCGGGCAAGTCAAGATAGAGATTAATTTGATCAGAGAAACCA 120
 QY 121 GAGACAGCTCTTAAGTGTCTCATTTTCTGGGCAATCAACCGGGAATCCGGGTCCTGAC 180
 DB 121 GAGACAGCTCTTAAGTGTCTCATTTTCTGGGCAATCAACCGGGAATCCGGGTCCTGAC 180
 QY 181 CGATTCAAGCGGCGATGATCTGGGCAAAATTAACCTCAACCTCAACCGGCGCT 240
 DB 181 CGATTCAAGCGGCGATGATCTGGGCAAAATTAACCTCAACCTCAACCGGCGCT 240
 QY 241 GAAGATTTTGTCTTACTTTTGTCAACAGTCTGACAGTTTGGCCGATCCTTCGGCCAA 300
 DB 241 GAAGATTTTGTCTTACTTTTGTCAACAGTCTGACAGTTTGGCCGATCCTTCGGCCAA 300
 QY 301 GGGACACGACTGGACATTCAA 321
 DB 301 GGGACACGACTGGACATTCAA 321

RESULT 5
 AAX77237
 ID AAX77237 standard; DNA; 321 BP.
 AC AAX77237;
 XX
 DT 04-AUG-1999 (first entry)
 DE Human kappa 8 light chain variable region encoding DNA.
 XX
 KM Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
 KW autoimmune disease; scFv-antibody; single-chain Fv; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9925818-A1.
 PD 27-MAY-1999.
 PF 16-NOV-1998; 98WO-EP007313.
 PR 17-NOV-1997; 97EP-00120096.
 PA (KUFE/) KUFEER P.
 XX
 PI Kufer P, Raum T, Borschert K, Zettl F, Lutterbuese R;
 XX
 DR WPI; 1999-338004/28.
 DR P-PSDB; AAY17955.
 XX
 PT Phase display system for identification of binding site domains retaining
 XX capacity to bind an epitope.
 PS Disclosure; Fig 3.2; 152p; English.
 XX
 CC The invention relates to a method of identifying binding site domains
 CC (BSD) that retain the capacity of binding to a predetermined epitope when
 CC positioned C-terminal of at least one further domain in a recombinant bi-
 CC or multivalent polypeptide. The method comprises (a) testing a panel of
 CC BSD displayed on the surface of a biological display system as part of a
 CC fusion protein for binding to a predetermined epitope, where the fusion
 CC protein comprises an additional domain positioned N-terminal of the BSD

CC and an amino acid sequence that mediates anchoring of the fusion protein
 CC to the surface of the display system; and (b) identifying a BSD that
 CC binds to the predetermined epitope. The method is useful to identify bi-
 CC or multivalent polypeptides that comprise antibody binding sites capable
 CC of efficiently binding to the corresponding antigen. The polypeptides or
 CC antibodies identified by the method are useful therapeutically and
 CC diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody
 CC fragments that bind independently of their position within bifunctional
 CC single-chain fusion proteins can be isolated from combinatorial antibody
 CC libraries using the new in vitro method

SQ Sequence 321 BP; 81 A; 91 C; 75 G; 74 T; 0 U; 0 Other;
 Query Match 81.1%; Score 260.2; DB 2; Length 321;
 Best Local Similarity 88.2%; Pred. No. 6.6e-74;
 Matches 283; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGATCTCCCTCTGTCATCTGTAGAGACAGATCACC 60
 DB 1 GAGCTCCAGATGACCCAGATCTCCCTCTGTCATCTGTAGAGACAGATCACC 60
 QY 61 ATCACTTGGCCGGGCAAGTCAAGATAGAGATTAATTTGATCAGAGAAACCA 120
 DB 61 ATCACTTGGCCGGGCAAGTCAAGATAGAGATTAATTTGATCAGAGAAACCA 120
 QY 121 GAGACAGCTCTTAAGTGTCTCATTTTCTGGGCAATCAACCGGGAATCCGGGTCCTGAC 180
 DB 121 GAGACAGCTCTTAAGTGTCTCATTTTCTGGGCAATCAACCGGGAATCCGGGTCCTGAC 180
 QY 181 CGATTCAAGCGGCGATGATCTGGGCAAAATTAACCTCAACCTCAACCGGCGCT 240
 DB 181 CGATTCAAGCGGCGATGATCTGGGCAAAATTAACCTCAACCTCAACCGGCGCT 240
 QY 241 GAAGATTTTGTCTTACTTTTGTCAACAGTCTGACAGTTTGGCCGATCCTTCGGCCAA 300
 DB 241 GAAGATTTTGTCTTACTTTTGTCAACAGTCTGACAGTTTGGCCGATCCTTCGGCCAA 300
 QY 301 GGGACACGACTGGACATTCAA 321
 DB 301 GGGACACGACTGGACATTCAA 321

RESULT 6
 ADOS1603
 ID ADOS1603 standard; DNA; 321 BP.
 AC ADOS1603;
 XX
 DT 15-JUL-2004 (first entry)
 DE Human TAG-72 antibody-related KCS18 gene SegID13.
 XX
 KM semi-human monoclonal antibody; tumour-associated glycoprotein antigen;
 KW TAG-72; human light chain; cancer; AK4; Hzk; VKI;
 KW human immunoglobulin kappa light chain germline; gene; de; human.
 XX
 OS Homo sapiens.
 XX
 EH Key
 FT CDS
 FT 1..321
 FT /tag= a
 FT /product= "Human TAG-72 antibody-related KCS18 protein"
 FT /partial
 FT /note= "No start or stop codon"
 XX
 PN KR2003013633-A.
 PD 15-FEB-2003.
 PF 08-AUG-2001; 2001KR-00047737.
 PR 08-AUG-2001; 2001KR-00047737.
 XX

PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Hong HJ, Kim SJ;
XX
DR WPI; 2003-500992/47.
DR P-PSDB; ADO51598.
XX
PT Semi-human monoclonal antibody binding to tumor-associated glycoprotein
PT antigen TAG-72 and human light chain comprising the same, useful for
PT diagnosing and treating cancer.
XX
PS Claim 13; SEQ ID NO 18; 1pp; Korean.
XX
CC This invention relates to a novel semi-human monoclonal antibody binding
CC to tumour-associated glycoprotein antigen TAG-72 and a human light chain
CC comprising the same. The semi-human monoclonal antibody has a human light
CC chain of which amino acid sequence is completely derived from the human,
CC therefore it is useful for the diagnosis and treatment of cancer. The
CC semi-human monoclonal antibody specifically binds to TAG-72 antigen of
CC which the light chain of human antibody AKA/HZK is substituted with the
CC light chain of a human derived antibody. The light chain of the human
CC derived antibody is preferably composed of amino acid sequence derived
CC from the VI family of the human immunoglobulin kappa light chain
CC germ-line. The present sequence is that of a gene which encodes a human
CC KCS protein which is related to the novel semi-human TAG-72 antibody of
CC the invention.
XX
SQ Sequence 321 BP; 87 A; 86 C; 73 G; 75 T; 0 U; 0 Other;
XX
Query Match 77.6%; Score 249; DB 11; Length 321;
Best Local Similarity 86.0%; Pred. No. 2.8e-70;
Matches 276; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
XX
QY 1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCACTGTAGAGACAGATCACC 60
Db 1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCACTGTAGAGACAGATCACC 60
XX
QY 61 ATCACTCTGGCCGGGCAAGTACAGACATTAGACAGTATTAAATTGGTATCAGCAAAACCA 120
Db 61 ATCACTCTGGCCGGGCAAGTACAGACATTAGACAGTATTAAATTGGTATCAGCAAAACCA 120
XX
QY 121 GGAACAGCCTCTTAAGTGTCTATTCTGGGCACTTACCCGGGAATCCGGGGTCCCTGAC 180
Db 121 GGAACAGCCTCTTAAGTGTCTATTCTGGGCACTTACCCGGGAATCCGGGGTCCCTGAC 180
XX
QY 181 CGATTTCAGGGGAGTGAATCTGGGCAAAATTACACTCTCAGCATCAGACCTGACGCT 240
Db 181 AGGTTTCAGGGGAGTGAATCTGGGCAAAATTACACTCTCAGCATCAGACCTGACGCT 240
XX
QY 241 GAAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTGGCGATCACTTGGCCCA 300
Db 241 GATGATTTTGTACTTACTTACTTGTCAACAGACTTACATTGCCCCCATCACTTGGCCCA 300
XX
QY 301 GGGACACGACCTGGACATTCAA 321
Db 301 GGGACACGACCTGGACATTCAA 321
XX
RESULT 7
AAL52122
ID AAL52122 standard; DNA; 324 BP.
XX
AC AAL52122;
XX
DT 29-MAY-2003 (first entry)
XX
DE Human anti-blood coagulation factor VIII antibody-related gene #4.
XX
KW Human; gene; db; anti-blood coagulation factor VIII antibody;
KW FVIII antibody; anti-thrombotic; thrombosis; activated FVIII.
OS Homo sapiens.
XX

FH Key Location/Qualifiers
FT CDS 1..324
FT FT /*tag= a
FT FT /partial
FT FT /product= "Human VIII antibody-related protein #4"
FT FT /note= "No start or stop codon is given"
XX
XX WO2002101040-A1.
XX
XX 19-DEC-2002.
XX
XX 11-JUN-2002; 2002WO-JP005783.
XX
XX 12-JUN-2001; 2001JP-00177640.
XX
XX (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
XX
XX Nakashima T, Yuguchi M;
XX
XX WPI; 2003-148804/14.
XX
XX P-PSDB; AAO16706.
XX
XX Human-type anti-blood coagulation factor VIII antibody, applicable in
XX PT antithrombotics for prevention or treatment of thrombosis, in diagnosis
XX PT of activated FVIII, and for maintaining low coagulation state.
XX
XX Disclosure; Page 28; 39pp; Japanese.
XX
XX The invention comprises the amino acid and coding sequence of a human
XX CC anti-blood coagulation factor VIII (FVIII) antibody, which has an
XX CC inhibitory activity on the coagulation activity of human FVIII. The
XX CC antibody is applicable in anti-thrombotics for prevention or treatment of
XX CC thrombosis, and in the diagnosis of activated FVIII. The present DNA
XX CC sequence encodes a human FVIII antibody-related protein
XX
SQ Sequence 324 BP; 87 A; 88 C; 73 G; 76 T; 0 U; 0 Other;
XX
Query Match 76.6%; Score 245.8; DB 10; Length 324;
Best Local Similarity 85.4%; Pred. No. 3.1e-69;
Matches 274; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
XX
QY 1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCACTGTAGAGACAGATCACC 60
Db 1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCACTGTAGAGACAGATCACC 60
XX
QY 61 ATCACTCTGGCCGGGCAAGTACAGACATTAGACAGTATTAAATTGGTATCAGCAAAACCA 120
Db 61 ATCACTCTGGCCGGGCAAGTACAGACATTAGACAGTATTAAATTGGTATCAGCAAAACCA 120
XX
QY 121 GGAACAGCCTCTTAAGTGTCTATTCTGGGCACTTACCCGGGAATCCGGGGTCCCTGAC 180
Db 121 GGAACAGCCTCTTAAGTGTCTATTCTGGGCACTTACCCGGGAATCCGGGGTCCCTGAC 180
XX
QY 181 CGATTTCAGGGGAGTGAATCTGGGCAAAATTACACTCTCAGCATCAGACCTGACGCT 240
Db 181 AGGTTTCAGGGGAGTGAATCTGGGCAAAATTACACTCTCAGCATCAGACCTGACGCT 240
XX
QY 241 GAAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTGGCGATCACTTGGCCCA 300
Db 241 GATGATTTTGTACTTACTTACTTGTCAACAGACTTACATTGCCCCCATCACTTGGCCCA 300
XX
QY 301 GGGACACGACCTGGACATTCAA 321
Db 301 GGGACACGACCTGGACATTCAA 321
XX
RESULT 8
AAH47727
ID AAH47727 standard; DNA; 342 BP.
XX
AC AAH47727;
XX
DT 30-NOV-2001 (first entry)
XX

```

XX  Nucleotide sequence of seq Id No. 70.
DE  Gene library; immunoglobulin; antibody library; human; ds.
XX  Homo sapiens.
XX  WO200162907-A1.
XX  30-AUG-2001.
XX  22-FEB-2001; 2001WO-JP001298.
XX  22-FEB-2000; 2000JP-00050543.
XX  (MED1-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX  Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M;
PI  Okuno Y, Shiraki K;
XX  WPI; 2001-565420/63.
XX  P-PSDB; AAG65563.
XX  Producing gene libraries and antibody libraries, involves selecting a
PT  light chain that binds to a heavy chain product to produce a functional
PT  formation, and producing a gene library of the light chain variable
XX  regions.
XX  Examples; p 146-147; 181pp; Japanese.
XX  The invention relates to producing gene libraries, comprising
CC  immunoglobulin light and heavy variable region. The method involves
CC  selecting light chain that binds with the heavy chain product to produce
CC  a functional conformation, producing a gene library comprising a
CC  collection of these light chain variable genes, and combining with gene
CC  library of heavy chain variable genes. The method is used for production
XX  of gene and antibody libraries
XX  Sequence 342 BP; 91 A; 93 C; 78 G; 80 T; 0 U; 0 Other;
SQ
Query Match      76.1%; Score 244.2; DB 4; Length 342;
Best Local Similarity 85.0%; Pred. No. 1e-68;
Matches 273; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY  1 GAGCTCAAGATGACCCAGTCTCCATCTCCCTGTCTGCACTCTGAGAGACAGATCACC 60
DB  1 GACATCGTATGACCCAGTCTCCATCTCCCTGTCTGCACTCTGAGAGACAGATCACC 60
QY  61 ATCACTTGGCCGGGCAAGTCAAGACATTAAGAGCTATTAAATTGATCAGAGAAACA 120
DB  61 ATCACTTGGCCGGGCAAGTCAAGACATTAAGAGCTATTAAATTGATCAGAGAAACA 120
QY  121 GGACAGCTCTTAAGTCTCATTTA CTGGGCATCTAACCCGGGAATCCGGGGTCCCTGAC 180
DB  121 GGGAAGACCCCTAAGTCTCATTTA CTGGGCATCTAACCCGGGAATCCGGGGTCCCTATCA 180
QY  181 CGATTAGCGGCGAGTGAATCTGGGACAAATTACATCTCAACATCGAGCCGCGAGCCT 240
DB  181 AGGTTCAAGTGGCAGTGAATCTGGGACAAATTACATCTCAACATCGAGCTCGCAACT 240
QY  241 GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCGATCCTTGGCCAA 300
DB  241 GAAGATTTTGTCAACTTACTTGTCAACAGATTAAGATTACAGTACCCGATCACTTGGCCAA 300
QY  301 GGGACACGACTGACATTCAA 321
DB  301 GGGACACGACTGAGATTAA 321

```

RESULT 9
AAH47731
ID AAH47731 standard; DNA; 321 BP.
XX

```

AC  AAH47731;
XX  30-NOV-2001 (First entry)
XX  Nucleotide sequence of seq Id No. 74.
DE  Gene library; immunoglobulin; antibody library; human; ds.
XX  Homo sapiens.
XX  WO200162907-A1.
XX  30-AUG-2001.
XX  22-FEB-2001; 2001WO-JP001298.
XX  22-FEB-2000; 2000JP-00050543.
XX  (MED1-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX  Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M;
PI  Okuno Y, Shiraki K;
XX  WPI; 2001-565420/63.
XX  P-PSDB; AAG65567.
XX  Producing gene libraries and antibody libraries, involves selecting a
PT  light chain that binds to a heavy chain product to produce a functional
PT  formation, and producing a gene library of the light chain variable
XX  regions.
XX  Examples; p 149; 181pp; Japanese.
XX  The invention relates to producing gene libraries, comprising
CC  immunoglobulin light and heavy variable region. The method involves
CC  selecting light chain that binds with the heavy chain product to produce
CC  a functional conformation, producing a gene library comprising a
CC  collection of these light chain variable genes, and combining with gene
CC  library of heavy chain variable genes. The method is used for production
XX  of gene and antibody libraries
XX  Sequence 321 BP; 87 A; 87 C; 72 G; 75 T; 0 U; 0 Other;
SQ
Query Match      75.6%; Score 242.6; DB 4; Length 321;
Best Local Similarity 84.7%; Pred. No. 3.4e-68;
Matches 272; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY  1 GAGCTCAAGATGACCCAGTCTCCATCTCCCTGTCTGCACTCTGAGAGACAGATCACC 60
DB  1 GACATCGTATGACCCAGTCTCCATCTCCCTGTCTGCACTCTGAGAGACAGATCACC 60
QY  61 ATCACTTGGCCGGGCAAGTCAAGACATTAAGAGCTATTAAATTGATCAGAGAAACA 120
DB  61 ATCACTTGGCCGGGCAAGTCAAGACATTAAGAGCTATTAAATTGATCAGAGAAACA 120
QY  121 GGACAGCTCTTAAGTCTCATTTA CTGGGCATCTAACCCGGGAATCCGGGGTCCCTGAC 180
DB  121 GGGAAGACCCCTAAGTCTCATTTA CTGGGCATCTAACCCGGGAATCCGGGGTCCCTATCA 180
QY  181 CGATTAGCGGCGAGTGAATCTGGGACAAATTACATCTCAACATCGAGCCGCGAGCCT 240
DB  181 AGGTTCAAGTGGCAGTGAATCTGGGACAAATTACATCTCAACATCGAGCTCGCAACT 240
QY  241 GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCGATCCTTGGCCAA 300
DB  241 GAAGATTTTGTCAACTTACTTGTCAACAGATTAAGATTACAGTACCCGATCACTTGGCCAA 300
QY  301 GGGACACGACTGACATTCAA 321
DB  301 GGGACACGACTGAGATTAA 321

```

RESULT 10

PI Huang H, Holmes S, Mason S;
 XX
 DR MPI; 2004-411694/38.
 DR P-PSDB; ADO36498.
 XX
 PT New human monoclonal antibody to heparanase, for use in treating or
 PT preventing cancer, autoimmune disease, arthritis, asthma, lupus
 PT erythematous, allograft rejection, atherosclerosis, and Alzheimer's
 PT disease.
 XX
 PS Claim 8; SEQ ID NO 11; 108bp; English.
 XX
 CC The present invention describes an isolated human monoclonal antibody
 CC which binds to and inhibits activity of human heparanase. Human anti-
 CC heparanase antibodies of the present invention have cytostatic,
 CC immunosuppressive, antiarthritic, antiasthmatic, antiinflammatory,
 CC dermatological, antiarteriosclerotic, neuroprotective and necrotic
 CC activities, and can be used as heparanase antagonists. The antibody,
 CC methods and compositions of the present invention are useful in treating
 CC or preventing cancer or tumors, e.g. melanoma, lymphoma, prostate
 CC carcinoma, pancreatic carcinoma, bladder carcinoma, fibrosarcoma,
 CC rhabdomyosarcoma, mastocytoma, mammary adenocarcinoma, leukaemia or a
 CC rheumatoid fibroblast, autoimmune disease, arthritis, asthma, lupus
 CC erythematous, allograft rejection, vascular restenosis, atherosclerosis,
 CC and Alzheimer's disease. The present sequence encodes a human anti-
 CC heparanase 13B2 v1 amino acid sequence, which is used in the
 CC exemplification of the present invention.
 CC
 XX
 SQ Sequence 321 BP; 81 A; 87 C; 76 G; 77 T; 0 U; 0 Other;
 XX
 Query Match 74.8%; Score 240.2; DB 12; Length 321;
 Best Local Similarity 84.9%; Pred. No. 26-67;
 Matches 269; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
 XX
 QY 5 TCCAGATGACCCAGTCTCCATCCCTGCTGTCATCTGTAGAGACAGAGTCAACATCA 64
 Db 5 TCCAGATTGACCCAGTCTCCATCCCTGCTGTCATCTGTAGAGACAGAGTCAACATCA 64
 QY 65 CTTCGCGGGCAAGTCAAGCATTAGACGCTATTAAATTGGTATCAGCAGAAACCCAGAC 124
 Db 65 CTTCGCGGGCAAGTCAAGCATTAGACGCTATTAAATTGGTATCAGCAGAAACCCAGAC 124
 QY 125 AGCCTCTTAAGCTGCTCATTTACTGAGCACTACCGGGGAATCCGGGGTCCCTGACCGAT 184
 Db 125 AGCCTCTTAAGCTGCTCATTTACTGAGCACTACCGGGGAATCCGGGGTCCCTGACCGAT 184
 QY 185 TCAGCGGAGTGAATCTGGGACAAATTACACTCTCAACATCAGACAGCTGACCTGAAG 244
 Db 185 TCAGCGGAGTGAATCTGGGACAAATTACACTCTCAACATCAGACAGCTGACCTGAAG 244
 QY 245 ATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTCCGATCACCCTTGGGCAAGGA 304
 Db 245 ATTTTGCAACTTACTTGTCTGCAACAGTTTAAATTAGTACCAGATCACCCTTGGGCAAGGA 304
 QY 305 CACGACTGGACATTCAA 321
 Db 305 CACGACTGGAGATTAAA 321
 XX
 RESULT 14
 ADD89879
 ID ADD89879 standard; cDNA; 327 BP.
 XX
 AC ADD89879;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human anti-TNF antibody 9C1A light chain variable region coding sequence.
 XX
 KW Human; Tumour necrosis factor; TNF; antibody; cytostatic; anabolic;
 KW eating-disorders-gen; immunomodulator; antimicrobial; cardiovascular-gen;
 KW neuroprotective; gene; ss.
 XX

OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH CDS 1..327
 FT /*tag= a
 FT /partial
 FT /product= "9C1A light chain variable region"
 FT /note= "No start or stop codon"
 XX
 XX MO2003083061-A2.
 XX
 XX PD 09-OCT-2003.
 XX
 XX 24-MAR-2003; 2003MO-US009072.
 XX
 XX 26-MAR-2002; 2002US-0367903P.
 XX
 XX (GEN2) CENTOCOR INC.
 XX
 XX Giles-Komar J, Scallion BJ, Carlton DM,
 XX
 XX MPI; 2003-804040/75.
 XX
 DR P-PSDB; ADD89870.
 XX
 PT New isolated mammalian anti-tumor necrosis factor (TNF) antibody, useful
 PT for diagnosing or treating an anti-TNF related condition, e.g. cancer,
 PT anorexia, cachexia, or bacterial infection.
 XX
 XX Example 4; Fig 3A; 87bp; English.
 XX
 CC The present sequence is the coding sequence of the light chain variable
 CC region of human anti-tumor necrosis factor (TNF) monoclonal antibody
 CC 9C1A. This human TNF reactive IgG monoclonal antibody was generated by
 CC cloning variable and constant region DNA in vector pC4 and expression in
 CC CHO cells. The invention provides isolated human, primate, rodent,
 CC mammalian, chimeric, humanized and/or CDR-grafted anti-TNF antibodies,
 CC immunoglobulins, their cleavage products, other specified portions and
 CC variants, as well as anti-TNF antibody compositions, nucleic acids
 CC encoding these, vectors, host cells, methods for producing the antibodies
 CC using a host cell, transgenic animal or transgenic plant or plant cell,
 CC and therapeutic compositions, methods and devices. The antibody, nucleic
 CC acid, protein, composition and methods are useful for diagnosing or
 CC treating an anti-TNF related condition, e.g. cancer, anorexia, cachexia,
 CC or an immune, cardiovascular, infectious, and/or neurological disease.
 CC
 XX
 SQ Sequence 327 BP; 84 A; 89 C; 76 G; 78 T; 0 U; 0 Other;
 XX
 Query Match 74.3%; Score 238.6; DB 10; Length 327;
 Best Local Similarity 84.5%; Pred. No. 6.7e-67;
 Matches 268; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
 XX
 QY 5 TCCAGATGACCCAGTCTCCATCCCTGCTGTCATCTGTAGAGACAGAGTCAACATCA 64
 Db 5 TCCAGATTGACCCAGTCTCCATCCCTGCTGTCATCTGTAGAGACAGAGTCAACATCA 64
 QY 65 CTTCGCGGGCAAGTCAAGCATTAGACGCTATTAAATTGGTATCAGCAGAAACCCAGAC 124
 Db 65 CTTCGCGGGCAAGTCAAGCATTAGACGCTATTAAATTGGTATCAGCAGAAACCCAGAC 124
 QY 125 AGCCTCTTAAGCTGCTCATTTACTGAGCACTACCGGGGAATCCGGGGTCCCTGACCGAT 184
 Db 125 AGCCTCTTAAGCTGCTCATTTACTGAGCACTACCGGGGAATCCGGGGTCCCTGACCGAT 184
 QY 185 TCAGCGGAGTGAATCTGGGACAAATTACACTCTCAACATCAGACAGCTGACCTGAAG 244
 Db 185 TCAGCGGAGTGAATCTGGGACAAATTACACTCTCAACATCAGACAGCTGACCTGAAG 244
 QY 245 ATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTCCGATCACCCTTGGGCAAGGA 304
 Db 245 ATTTTGCAACTTACTTGTCTGCAACAGTTTAAATTAGTACCAGATCACCCTTGGGCAAGGA 304
 QY 305 CACGACTGGACATTCAA 321
 Db 305 CACGACTGGAGATTAAA 321
 XX

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 05:42:24, Search time 66.271 Seconds
(without alignments)
3442.884 Million cell updates/sec

Title: US-09-403-107-147

Perfect score: 321
Sequence: 1 gggcccgagatgacccagtc.....ggagacagctggaattcaa 321

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
4: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfileseq1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	240.8	75.0	321	3	US-09-240-274-106
2	236.2	73.6	321	2	US-08-378-939-13
3	231.4	72.1	720	4	US-09-192-854-1
4	228.2	71.1	714	4	US-09-472-087-62
5	224	69.8	321	3	US-09-240-274-216
6	223.2	69.5	321	3	US-09-240-274-102
7	223.2	69.5	321	3	US-09-240-274-109
8	223.2	69.5	321	3	US-09-240-274-215
9	223.2	69.5	321	3	US-09-240-274-217
10	223.2	69.5	321	3	US-09-240-274-218
11	221.6	69.0	321	3	US-09-240-274-199
12	220.2	68.6	388	3	US-09-042-353-358
13	220.2	68.6	388	3	US-08-758-417A-206
14	220	68.5	321	3	US-09-240-274-107
15	218.4	68.0	321	3	US-09-240-274-211
16	218.4	68.0	321	3	US-09-240-274-221
17	218.4	68.0	321	3	US-09-240-274-222
18	217.8	67.9	451	4	US-09-472-087-50
19	217	67.6	439	3	US-09-042-353-360
20	217	67.6	439	3	US-08-758-417A-208
21	216.8	67.5	321	3	US-09-240-274-201
22	216.2	67.4	672	4	US-09-456-090A-47
23	216.2	67.4	672	4	US-09-453-234-47
24	216	67.3	321	3	US-09-240-274-205
25	215.4	67.1	324	2	US-08-378-939-31
26	215.4	67.1	324	2	US-08-378-939-33
27	215.4	67.1	387	3	US-08-803-085-3

28	215.4	67.1	19040	4	US-09-343-485A-3	Sequence 3, Appl
29	215.2	67.0	321	3	US-09-240-274-105	Sequence 105, App
30	215.2	67.0	321	3	US-09-240-274-113	Sequence 113, App
31	213.8	66.6	324	2	US-08-378-939-17	Sequence 17, Appl
32	213.8	66.6	420	3	US-09-042-353-420	Sequence 420, App
33	213.8	66.6	420	3	US-08-758-417A-220	Sequence 220, Appl
34	213.8	66.6	3819	3	US-09-042-353-393	Sequence 393, App
35	213.8	66.6	3819	3	US-08-758-417A-243	Sequence 243, App
36	213.6	66.5	321	3	US-09-240-274-108	Sequence 108, App
37	213.6	66.5	321	3	US-09-240-274-203	Sequence 203, App
38	213.6	66.5	402	2	US-09-472-087-49	Sequence 49, Appl
39	213.2	66.4	390	2	US-08-646-367-2	Sequence 2, Appl
40	212.2	66.1	321	2	US-08-488-376-12	Sequence 12, Appl
41	212.2	66.1	321	2	US-08-634-223-12	Sequence 12, Appl
42	212.2	66.1	321	2	US-08-634-224-12	Sequence 12, Appl
43	212.2	66.1	321	2	US-08-634-400-12	Sequence 12, Appl
44	212.2	66.1	321	2	US-08-635-878-12	Sequence 12, Appl
45	212.2	66.1	321	2	US-08-770-057-12	Sequence 12, Appl

ALIGNMENTS

```
RESULT 1
US-09-240-274-106
Sequence 106, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 106
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain 106
US-09-240-274-106

Query Match      75.0%; Score 240.8; DB 3; Length 321;
Best Local Similarity 85.1%; Pred. No. 1.1e-72;
Matches 269; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY      6  CCAGATGACCCAGTCTGCATCTCCCTGTCGATCTGTAGAGACAGATCACCATCAC 65
DB      3  CAGAGTCACCCAGTCTGCATCTCCCTGTCGATCTGTAGAGACAGATCACCATCAC 62
QY      66  TTGCGCGGCAAGTCAGAGCATTTGAATTTGATTCAGACAGAACAGAGACA 125
DB      63  TTGCGCGGCAAGTCAGAGCATTTGAATTTGATTCAGACAGAACAGAGACA 122
QY      126  GCGCTTAGAGTCGATCTTACTGCGGATCTCCCGGGAATCCGGGGTCCCTGACGATT 185
DB      123  AGCCCTTAGAGTCGATCTTACTGCGGATCTCCCGGGAATCCGGGGTCCCTGACGATT 182
QY      186  CAGCGGAGTGAATCTGGAGCAATATACCTCTCAGCATCAGAGCCTCAGCCTGAAGA 245
DB      183  CAGTGCATGATCTGGAGCAAGATTTACTCTCAGCATCAGAGCTGCAACTGAAGA 242
QY      246  TTTTGCTACTTACTTTTGCAACAGTCTGACAGTTTGGCGATCCTTGCGCCAGGAGC 305
DB      243  TTTTGCAACTTACTTGTCAACAGAGTTACAGATCCGATCACCCTTGCGCCAGGAGC 302
QY      306  AGAGCTGACATTCMA 321
```

Db 303 AGACTGGAGATTAAA 318

RESULT 2

US-08-378-939-13

Sequence 13, Application US/08378939

Patent No. 5876961

GENERAL INFORMATION:

APPLICANT: CROME, JAMES SCOTT

APPLICANT: LEWIS, ALAN PETER

TITLE OF INVENTION: PRODUCTION OF ANTIBODIES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ

STREET: 555 THIRTEENTH ST. N.W.

CITY: WASHINGTON

STATE: D. C.

COUNTRY: U.S.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/378,939

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/952640

FILING DATE: 01-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: ERNST, BARBARA G

REGISTRATION NUMBER: 30,377

REFERENCE/DOCKET NUMBER: 1808-118

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 783-6040

TELEFAX: (202) 783-6031

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 321 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 1..321

US-08-378-939-13

Query Match

Best Local Similarity 83.5%; Pred. No. 4e-71;

Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Db 1 GAGCTCCAGATGACCCAGTCTCATCTCCCTGCTGCTGATAGGAGACAGATCACC 60

Db 1 GACATTCACATAGACCCAGTCTCATCTCCCTGCTGCTGATAGGAGACAGATCACC 60

Db 61 ATCACTTGGCGGGGCAAGTACAGACATTAATTAATTTGATCAGAGAAACCA 120

Db 61 ATCACTTGGCGGGGCAAGTACAGACATTAATTAATTTGATCAGAGAAACCA 120

Db 61 ATCACTTGGCGGGGCAAGTACAGACATTAATTAATTTGATCAGAGAAACCA 120

Db 121 GGAAGAGCTCTTAAGTCTCATTTACTGGGATCTACCCGGGATCCCTGAC 180

Db 121 GGAAGAGCTCTTAAGTCTCATTTACTGGGATCTACCCGGGATCCCTGAC 180

Db 121 GGAAGAGCTCTTAAGTCTCATTTACTGGGATCTACCCGGGATCCCTGAC 180

Db 121 GGAAGAGCTCTTAAGTCTCATTTACTGGGATCTACCCGGGATCCCTGAC 180

Db 181 CGATTGAGGGGAGGATCTGGGCAATTAACCTCAGACAGAGAGCTGAGAGCT 240

Db 181 CGATTGAGGGGAGGATCTGGGCAATTAACCTCAGACAGAGAGCTGAGAGCT 240

Db 181 AGGTTCAGTGGAGTGGATCTGGGACAGACTTCACTCAGCAGAGCTGCAACCT 240

Db 181 AGGTTCAGTGGAGTGGATCTGGGACAGACTTCACTCAGCAGAGCTGCAACCT 240

Qy 241 GAAGATTTTGTACTTACTTTTGTCAACAGCTGACAGTTTCCGATCACCCTTGGCCAA 300

Db 241 GAAGATTTTGTCAACTTACTTACTTGTCAACAGATTAAGTACCTGATCACCCTTGGCCAA 300

Qy 301 GGGACAGCAGCTGGACATTCAA 321

Db 301 GGGACAGCAGCTGGAGATTAAA 321

RESULT 3

US-09-192-854-1

Sequence 1, Application US/09192854

Patent No. 6696245

GENERAL INFORMATION:

APPLICANT: Tomlinson, Ian

APPLICANT: Winter, Greg

TITLE OF INVENTION: Methods for Selecting Functional Peptides

FILE REFERENCE: 3789/72916

CURRENT APPLICATION NUMBER: US/09/192,854

EARLIER FILING DATE: 1998-11-17

EARLIER FILING DATE: 1997-11-21

NUMBER OF SEQ ID NOS: 212

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 720

TYPE: DNA

ORGANISM: Homo sapiens

US-09-192-854-1

Query Match

Best Local Similarity 72.1%; Score 231.4; DB 4; Length 720;

Matches 265; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 1 GAGCTCCAGATGACCCAGTCTCATCTCCCTGCTGCTGATAGGAGACAGTCAAC 60

Db 397 GACATTCACATAGACCCAGTCTCATCTCCCTGCTGCTGATAGGAGACAGTCAAC 456

Qy 61 ATCACTTGGCGGGGCAAGTACAGACATTAATTAATTTGATCAGAGAAACCA 120

Db 457 ATCACTTGGCGGGGCAAGTACAGACATTAATTAATTTGATCAGAGAAACCA 516

Qy 121 GGAAGAGCTCTTAAGTCTCATTTACTGGGATCTACCCGGGATCCCTGAC 180

Db 517 GGAAGAGCTCTTAAGTCTCATTTACTGGGATCTACCCGGGATCCCTGAC 576

Qy 181 CGATTGAGGGGAGGATCTGGGCAATTAACCTCAGACAGAGAGCTGAGAGCT 240

Db 577 AGGTTCAGTGGAGTGGATCTGGGACAGATTTCACATCAGCAGTGTGCAACT 636

Qy 241 GAAATTTTGTACTTACTTTTGTCAACAGCTGACAGTTTGGCCGATCACCCTTGGCCAA 300

Db 637 GAAATTTTGTACTTACTTTTGTCAACAGCTGACAGTTTGGCCGATCACCCTTGGCCAA 696

Qy 301 GGGACAGCAGCTGGACATTCAA 321

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

Db 697 GGGACAGCAGCTGGAAATCAA 717

CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 62
LENGTH: 714
TYPE: DNA
ORGANISM: Homo sapiens
US-09-472-087-62

Query Match 71.1%; Score 228.2; DB 4; Length 714;
Best Local Similarity 81.9%; Pred. No. 3.2e-68;
Matches 263; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTGATCTGTAGAGACAGAGTACC 60
DB 67 GACATCCAGATGACCCAGTCTCCATCTCCCTGCTGATCTGTAGAGACAGAGTACC 126
QY 61 ATCACTGCGGCGAGATGAGACATTTAGAGCATTTTAATTGGTATCAGAGAAACA 120
DB 127 ATCACTGCGGCGAGATGAGACATTTAGAGCATTTTAATTGGTATCAGAGAAACA 186
QY 121 GAGACGCTCTAGCTGCTCATTTTACTGGGATCTACCCGGGAATCCGGGGTCCCTGAC 180
DB 187 GGGAAAGCCCTTAATCTCTGATCTATGCTGATCCAGTTTGGAAAGTGGGTCCTATCA 246
QY 181 CGATTCAGCGGAGATGATCTGGGACAAATTAACACTCTACATCAGACCTGACGCT 240
DB 247 AGTTCAGTGGGAGATGATCTGGGACAAATTAACACTCTACATCAGACCTGACGCT 306
QY 241 GAAATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCGATCACTTGGCCAA 300
DB 307 GAAATTTTGTCAACTACTCTCAACAGTATTAAGATCTTCACTTTCGGCCCT 366
QY 301 GGGACACGCTGACATTTCA 321
DB 367 GGGACCAAGTGAATCAAA 387

RESULT 5
US-09-240-274-216
Sequence 216, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 216
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH47
US-09-240-274-216

Query Match 69.8%; Score 224; DB 3; Length 321;
Best Local Similarity 82.4%; Pred. No. 6.1e-67;
Matches 257; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 6 CGAGTATGACCCAGTCTCCATCTCTGCTGATCTGTAGAGACAGAGTACCATCAG 65
DB 3 CGAGTATGACCCAGTCTCCATCTCTGCTGATCTGTAGAGACAGAGTACCATCAG 62

QY 66 TTGCCGGGCAAGTCAAGATTTAGAGCATTTAATTGGTATCAGAGAAACAAGACA 125
DB 63 TTGCCGGGCAAGTCAAGATTTAGAGCATTTAATTGGTATCAGAGAAACAAGACA 122
QY 126 GCTCTTAAGTCTCATTTTACTGGGATCTACCCGGGATCCGGGGTCCCTGACGAT 185
DB 123 AGCCCTTAAGTCTCATTTTACTGGGATCTACCCGGGATCCGGGGTCCCTGACGAT 182
QY 186 CAGCGGAGTGAATCTGGGACAAATTAACACTCAACATCAGACGCTGACCTGAGAGA 245
DB 183 CAGTGGAGTGAATCTGGGACAAATTAACACTCAACATCAGACGCTGACCTGAGAGA 242
QY 246 TTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCGATCCTTGGCGAAGGAC 305
DB 243 TTTTGTCACTTACTCTGTCAACAGATTTAGAGTATCTCTGCGAGTTTGGCGAAGGAC 302
QY 306 ACGACTGACAT 317
DB 303 CAGGTGAGAT 314

RESULT 6
US-09-240-274-102
Sequence 102, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 102
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain 102
US-09-240-274-102

Query Match 69.5%; Score 223.2; DB 3; Length 321;
Best Local Similarity 81.6%; Pred. No. 1.1e-66;
Matches 258; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
QY 6 CGAGTATGACCCAGTCTCCATCTCTGCTGATCTGTAGAGACAGAGTACCATCAG 65
DB 3 CGAGTATGACCCAGTCTCCATCTCTGCTGATCTGTAGAGACAGAGTACCATCAG 62
QY 66 TTGCCGGGCAAGTCAAGATTTAGAGCATTTAATTGGTATCAGAGAAACAAGACA 125
DB 63 TTGCCGGGCAAGTCAAGATTTAGAGCATTTAATTGGTATCAGAGAAACAAGACA 122
QY 126 GCTCTTAAGTCTCATTTTACTGGGATCTACCCGGGATCCGGGGTCCCTGACGAT 185
DB 123 AGCCCTTAAGTCTCATTTTACTGGGATCTACCCGGGATCCGGGGTCCCTGACGAT 182
QY 186 CAGCGGAGTGAATCTGGGACAAATTAACACTCAACATCAGACGCTGACCTGAGAGA 245
DB 183 CAGTGGAGTGAATCTGGGACAAATTAACACTCAACATCAGACGCTGACCTGAGAGA 242
QY 246 TTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCGATCCTTGGCGAAGGAC 305
DB 243 TTTTGTCACTTACTCTGTCAACAGATTTAGAGTATCTCTGCGAGTTTGGCGAAGGAC 302
QY 306 ACGACTGACATCA 321

Db 63 TTGCCGGGCAAGTCAGTACATTAAGACGTATTTAAATGGTATCAGAGAAACAGGAA 122
126 GCCTCTAAGCTCTCTATTTACTGGGATATACCCGGGATCCGGGGTCCCTTACCAT 185
Db 123 AGCCCTTAATCTCTGATATGCTGATCCAGTTTGCAAGGGGGTCCCATCAAGTT 182
Qy 186 CAGCGGAGATGTCGGGCAAAATTAACACTCTCAGCATGAGAGCCTGAGCCTGAGA 245
183 CAGTGGCAGTGTCTGGGACAGATTTCACTCTCAGCATGAGAGTCTGCAACCTGAGA 242
Qy 246 TTTTGCTACTTCTTTTGTCAACAGTCTGACAGTTGGCCGATCACTTGGCCCAAGGAC 305
Db 243 TTTTGCACTTACTACTGTCAACAGACTTACAGTTCCCTGAGACCTTTGGCCCTGGAC 302
Qy 306 AGCACTGACATTCAA 321
Db 303 CAAGTGAGATCAAA 318

RESULT 10

US-09-240-274-218
Sequence 218, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
EARLIER FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 218
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-240-274-218

Query Match 69.5%; Score 223.2; DB 3; Length 321;
Best Local Similarity 81.6%; Pred. No. 1.1e-66;
Matches 258; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 6 CCAGATGACCCAGTCTCCATCCCTCCCTGTGATCTGTAGAGACAGAGTCCATCAC 65
Db 3 CGAGCTCACCCAGTCTCCATCCCTCCCTGTGATCTGTAGAGACAGAGTCCATCAC 62
Qy 66 TTGCCGGGCAAGTCAGATGTCAGAGTATTTAAATGGTATCAGAGAAACAGAGAC 125
Db 63 TTGCCGGGCAAGTCAGATGTCAGAGTATTTAAATGGTATCAGAGAAACAGAGAC 122
Qy 126 GCCTCTAAGCTCTCTATTTACTGGGATATACCCGGGATCCGGGGTCCCTTACCGATT 185
Db 123 AGCCCTTAATCTCTGATATGCTGATCCAGTTTGCAAGGGGGTCCCATCAAGTT 182
Qy 186 CAGCGGAGATGTCGGGCAAAATTAACACTCTCAGCATGAGAGCCTGAGCCTGAGA 245
Db 183 CAGTGGCAGTGTCTGGGACAGATTTCACTCTCAGCATGAGAGTCTGCAACCTGAGA 242
Qy 246 TTTTGCTACTTCTTTTGTCAACAGTCTGACAGTTGGCCGATCACTTGGCCCAAGGAC 305
Db 243 TTTTGCACTTACTACTGTCAACAGACTTACAGTTCCCTGAGACCTTTGGCCCTGGAC 302
Qy 306 AGCACTGACATTCAA 321
Db 303 CAAGTGAGATCAAA 318

RESULT 11

US-09-240-274-199
Sequence 199, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
EARLIER FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 199
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-240-274-199

Query Match 69.0%; Score 221.6; DB 3; Length 321;
Best Local Similarity 81.3%; Pred. No. 4e-66;
Matches 257; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

Qy 6 CCAGATGACCCAGTCTCCATCCCTCCCTGTGATCTGTAGAGACAGAGTCCATCAC 65
Db 3 CGAGCTCACCCAGTCTCCATCCCTCCCTGTGATCTGTAGAGACAGAGTCCATCAC 62
Qy 66 TTGCCGGGCAAGTCAGATGTCAGAGTATTTAAATGGTATCAGAGAAACAGAGAC 125
Db 63 TTGCCGGGCAAGTCAGATGTCAGAGTATTTAAATGGTATCAGAGAAACAGAGAC 122
Qy 126 GCCTCTAAGCTCTCTATTTACTGGGATATACCCGGGATCCGGGGTCCCTTACCGATT 185
Db 123 AGCCCTTAATCTCTGATATGCTGATCCAGTTTGCAAGGGGGTCCCATCAAGTT 182
Qy 186 CAGCGGAGATGTCGGGCAAAATTAACACTCTCAGCATGAGAGCCTGAGCCTGAGA 245
Db 183 CAGTGGCAGTGTCTGGGACAGATTTCACTCTCAGCATGAGAGTCTGCAACCTGAGA 242
Qy 246 TTTTGCTACTTCTTTTGTCAACAGTCTGACAGTTGGCCGATCACTTGGCCCAAGGAC 305
Db 243 TTTTGCACTTACTACTGTCAACAGACTTACAGTTCCCTGAGACCTTTGGCCCTGGAC 302
Qy 306 AGCACTGACATTCAA 321
Db 303 CAAGTGAGATCAAA 318

RESULT 12

US-09-042-353-358
Sequence 358, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESSES:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 016643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ. ID NO. 358:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-042-353-358

Query Match 68.6%; Score 220.2; DB 3; Length 388;
Best Local Similarity 80.4%; Pred. No. 1.3e-65;

Matches 258; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCTCTGTCGATCTGTAGAGACAGTCAAC 60
DB 67 GACATTCAGATGACCCAGTCTCCATCTCTCTGTCGATCTGTAGAGACAGTCAAC 126
QY 61 ATCACTTCCCGGCAAGTCAGAGCATTTAGGAGCTATTTAAATTGGATTCAGAGAAACA 120
DB 127 ATCACTTCCCGGCAAGTCAGAGCATTTAGGAGCTATTTAAATTGGATTCAGAGAAACA 186
QY 121 GACAGCCTCTTAAGCTGCTATTACTGCGGATCTACCCGGAATCCGGGCTCTGAC 180
DB 187 GGGAAAGCCCTTAAGCTGCTATTACTGCGGATCTACCCGGAATCCGGGCTCTGAC 246
QY 181 CGATTTCAGGCGAGTGAATCTGGACAAATTACATCTTCACCATATGACAGCTTCAGCCT 240
DB 247 AGGTTTCAGGCGAGTGAATCTGGACAAATTACATCTTCACCATATGACAGCTTCAGCCT 306
QY 241 GAAATTTTGTACTTACTTTGTACACAGTGTGACAGTTTGGCATCACTTCGCGCA 300
DB 307 GAAATTTTGTACTTACTTTGTACACAGTGTGACAGTTTGGCATCACTTCGCGCA 366
QY 301 GGGACAGCATGAGCATTCAA 321
DB 367 GGGACAGCATGAGCATTCAA 387

RESULT 13
US-08-758-417A-206
; Sequence 206, Application US/08758417A
; Patent No. 6300129
; GENERAL INFORMATION:
; APPLICANT: Lomborg, Nils
; Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
; Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 417
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,417A
; FILING DATE: 02-DEC-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/728,463
; FILING DATE: 10-OCT-1996
; APPLICATION NUMBER: US 08/544,404
; FILING DATE: 10-OCT-1995
; APPLICATION NUMBER: US 08/352,322
; FILING DATE: 07-DEC-1994
; APPLICATION NUMBER: US 08/209,741
; FILING DATE: 09-MAR-1994
; APPLICATION NUMBER: US 08/165,699
; FILING DATE: 10-DEC-1993
; APPLICATION NUMBER: US 08/161,739
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: US 08/155,301
; FILING DATE: 18-NOV-1993
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; APPLICATION NUMBER: US 07/990,860

FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 206:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-08-758-417A-206

Query Match 68.6%; Score 220.2; DB 3; Length 388;
Best Local Similarity 80.4%; Pred. No. 1.3e-65;
Matches 258; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCCTGTCGATCTGTAGAGACAGAGTACC 60
DB 67 GACATCCAGATGACCCAGTCTCCCTGTCGATCTGTAGAGACAGAGTACC 126
QY 61 ATCACTTCCGGGCAAGTCAAGCATTAGAGCTATTAAATTGGTATCAGCAAAACA 120
DB 127 ATCACTTCCGGGCAAGTCAAGCATTAGAGCTATTAAATTGGTATCAGCAAAACA 186
QY 121 GAGACCTCTTAAAGTCTCTTCTGCGCATCTACCCGGGAATCCGGGTCCTGAC 180
DB 187 GGGAAAGCCCTTAAGCTCTGATCTATGTCGATCTCAAGTTGAAAGTGGGTCCTCA 246
QY 181 CGATTGAGGCGGAGTATCTGGGCAAAATTACCTCTCACTCAAGACCTGACGCT 240
DB 247 AGGTTGAGGCGGAGTATCTGGGCAAAATTACCTCTCACTCAAGACCTGACGCT 306
QY 241 GAAAGTTTGTCTTACTTTTGTCAACAGTCTGACAGTTTGGCCATCAGCTTGGCCAA 300
DB 307 GAAAGTTTGTCTTACTTTTGTCAACAGTCTGACAGTTTGGCCATCAGCTTGGCCAG 366
QY 301 GGGACGACGCTGACATTCGA 321
DB 367 GGGACGACGCTGACATTCGA 387

RESULT 14

US-09-240-274-107
Sequence 107, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 107
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain I07
US-09-240-274-107

Query Match 68.5%; Score 220; DB 3; Length 321;

Best Local Similarity 81.0%; Pred. No. 1.4e-65;
Matches 256; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 6 CCAGATGACCCAGTCTCCCTGTCGATCTGTAGAGACAGAGTACC 65
DB 3 CGAGTCAACCCAGTCTCCCTGTCGATCTGTAGAGACAGAGTACC 62
QY 66 TTGCGGCGGCAAGTCAAGCATTAGAGCTATTAAATTGGTATCAGCAAAACCAGACA 125
DB 63 TTGCGGCGGCAAGTCAAGCATTAGAGCTATTAAATTGGTATCAGCAAAACCAGGAA 122
QY 126 GCCTCCCTAAGCTCTGATTTTACTGCGCATCTACCCGGGAATCCGGGTCCTGACGATT 185
DB 123 AGCCCTTAAGCTCTGATTTTACTGCGCATCTACCCGGGAATCCGGGTCCTGACGATT 182
QY 186 CAGCGGCGGCAAGTCTGCGGCAAAATTACCTCTCACTCAAGACCTGACGCTGAGA 245
DB 183 CAGTGGCAGTGTATCTGGGCAAGATTCTCTCACTCAAGACCTGACGCTGAGA 242
QY 246 TTTTGTCTTACTTTTGTCAACAGTCTGACAGTTTGGGATACCTTGGCCAAAGGAC 305
DB 243 TTTTGTCTTACTTTTGTCAACAGTCTGACAGTTTGGGATACCTTGGCCAAAGGAC 302
QY 306 ACGACTGACATTCGA 321
DB 303 CAAAGTGGAGATCAGA 318

RESULT 15

US-09-240-274-211
Sequence 211, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 211
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH36
US-09-240-274-211

Query Match 68.0%; Score 218.4; DB 3; Length 321;
Best Local Similarity 80.7%; Pred. No. 5e-65;
Matches 255; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 6 CCAGATGACCCAGTCTCCCTGTCGATCTGTAGAGACAGAGTACC 65
DB 3 CGAGTCAACCCAGTCTCCCTGTCGATCTGTAGAGACAGAGTACC 62
QY 66 TTGCGGCGGCAAGTCAAGCATTAGAGCTATTAAATTGGTATCAGCAAAACCAGACA 125
DB 63 TTGCGGCGGCAAGTCAAGCATTAGAGCTATTAAATTGGTATCAGCAAAACCAGGAA 122
QY 126 GCCTCCCTAAGCTCTGATTTTACTGCGCATCTACCCGGGAATCCGGGTCCTGACGATT 185
DB 123 AGCCCTTAAGCTCTGATTTTACTGCGCATCTACCCGGGAATCCGGGTCCTGACGATT 182
QY 186 CAGCGGCGGCAAGTCTGCGGCAAAATTACCTCTCACTCAAGACCTGACGCTGAGA 245
DB 183 CAGTGGCAGTGTATCTGGGCAAGATTCTCTCACTCAAGACCTGACGCTGAGA 242

Qy	246	TTTTGCTACTTACTTTTGTCACAGTCTGACAGTTTGCCGATCCTTGGCCCAAGGAC	305
Db	243	TTTTGCACTTACTACTGTCAACAGATTACAGTACCCCTCCGGCTTTCGGCCCTGGGAC	302
Qy	306	ACGACTGACATTCAA	321
Db	303	CAAAGTGAATTCAA	318

Search completed: December 7, 2004, 08:57:56
 Job time : 67.271 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: December 7, 2004, 08:53:09 ; Search time 275.899 Seconds
(without alignments)
6393.344 Million cell updates/sec

Title: US-09-403-107-147

Perfect score: 321

Sequence: 1 ggcctccagatgaccacgctc.....ggacacgactggacattcaa 321

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3695051 seqs, 2747533894 residues

Total number of hits satisfying chosen parameters: 7390102

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	321	100.0	321	15	US-10-325-694-147
2	255.4	79.6	321	15	US-10-325-694-141
3	245.8	79.6	324	17	US-10-344-514-7
4	245.8	75.0	324	17	US-10-344-514-8
5	240.8	75.0	321	17	US-09-848-798-106
6	240.2	74.8	321	17	US-10-703-714-11
7	240.2	74.8	321	17	US-10-703-714-11
8	239.4	74.6	322	16	US-10-309-762-215
9	239.4	74.6	322	16	US-10-309-762-228
10	236.2	73.6	322	16	US-10-309-762-213
11	236.2	73.6	322	16	US-10-309-762-238
12	235	73.2	1106	16	US-10-264-049-121

13	231.4	72.1	333	15	US-10-203-754A-60	Sequence 60, App1
14	231.4	72.1	720	9	US-09-192-854-1	Sequence 1, App1
15	231.4	72.1	720	9	US-09-968-561A-1	Sequence 1, App1
16	231.4	72.1	720	10	US-09-968-744A-1	Sequence 1, App1
17	231.4	72.1	720	11	US-09-968-561A-1	Sequence 1, App1
18	231.4	72.1	720	18	US-10-744-774-2	Sequence 2, App1
19	231.4	72.1	900	15	US-10-203-754A-64	Sequence 64, App1
20	229.8	71.6	321	16	US-10-338-366-11	Sequence 11, App1
21	229.8	71.6	324	17	US-10-344-514-3	Sequence 3, App1
22	229.8	71.6	324	17	US-10-344-514-4	Sequence 4, App1
23	229.8	71.6	729	15	US-10-216-484-125	Sequence 125, App
24	229.8	71.6	729	15	US-10-384-933-125	Sequence 125, App
25	228.2	71.1	322	16	US-10-309-762-226	Sequence 226, App
26	228.2	71.1	322	16	US-10-309-762-227	Sequence 227, App
27	228.2	71.1	324	18	US-10-409-814A-3	Sequence 3, App1
28	228.2	71.1	714	14	US-10-153-382-18	Sequence 18, App1
29	228.2	71.1	714	18	US-10-612-497-62	Sequence 62, App1
30	228.2	71.1	714	18	US-10-776-649-62	Sequence 62, App1
31	228.2	71.1	819	14	US-10-158-646-65	Sequence 65, App1
32	226.6	70.6	322	15	US-10-041-860-74	Sequence 74, App1
33	226.6	70.6	322	16	US-10-309-762-221	Sequence 221, App
34	226.6	70.6	322	16	US-10-309-762-233	Sequence 233, App
35	226.6	70.6	322	17	US-10-665-383-43	Sequence 43, App1
36	226.6	70.6	463	16	US-10-395-894-20	Sequence 20, App1
37	226.6	70.6	463	17	US-10-695-667-20	Sequence 20, App1
38	226.6	70.6	514	14	US-10-066-543-2025	Sequence 2025, App
39	226.6	70.6	537	14	US-10-066-543-186	Sequence 186, App
40	226.6	70.6	6082	16	US-10-395-894-9	Sequence 9, App1
41	226.6	70.6	6082	17	US-10-695-667-9	Sequence 9, App1
42	225.8	70.3	321	14	US-10-073-644C-3	Sequence 3, App1
43	225.4	70.2	322	16	US-10-038-591-54	Sequence 54, App1
44	225.4	70.1	322	18	US-10-775-444A-54	Sequence 54, App1
45	225	70.1	321	15	US-10-091-300-42	Sequence 42, App1

ALIGNMENTS

RESULT 1

US-10-325-694-147

Sequence 147, Application US/10325694

Publication No. US20030148463A1

GENERAL INFORMATION:

APPLICANT: KUPER, PETER

APPLICANT: RAUM, TOBIAS

TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN

FILE REFERENCE: 38164000

CURRENT APPLICATION NUMBER: US/10/325,694

CURRENT FILING DATE: 2002-12-19

PRIOR APPLICATION NUMBER: US/09/403,107

PRIOR FILING DATE: 1999-10-14

NUMBER OF SEQ ID NOS: 152

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 147

LENGTH: 321

TYPE: DNA

ORGANISM: HUMAN

US-10-325-694-147

Query Match 100.0%; Score 321; DB 15; Length 321;

Best Local Similarity 100.0%; Pred. No. 2.9e-101; Indels 0; Gaps 0;

Matches 321; Conservative 0; Mismatches 0;

QY	1	GAGCTCCAGATGACCCAGCTCCATCCCTGCTGCACTGTAGAGACAGAGTCACC	60
DB	1	GAGCTCCAGATGACCCAGCTCCATCCCTGCTGCACTGTAGAGACAGAGTCACC	60
QY	61	ATCACTTCCGCGGCAAGTCAAGACATTAACAGCTATTAAATTGATACAGAGAACCA	120
DB	61	ATCACTTCCGCGGCAAGTCAAGACATTAACAGCTATTAAATTGATACAGAGAACCA	120
QY	121	GGACACCTCTCTAAGTGTCTATTCTGGGATCTACCCGGGAATCCGGGGTCCCTGAC	180

```

Db      121  GGACACCTCTCTAAGCTGCTCATTTTACTGGGATCTACCCGGGAATCCGGGCTCCCTGAC 180
QY      181  CGATTAGGGGCGAGTATCTGGGACAAATTACACTCTGCACCTAGCAGCTTGAGCCT 240
Db      181  CGATTAGGGGCGAGTATCTGGGACAAATTACACTCTGCACCTAGCAGCTTGAGCCT 240
QY      241  GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCGATCACTTGGCCAA 300
Db      241  GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCGATCACTTGGCCAA 300
QY      301  GGGACACGACTGGACATTCAA 321
Db      301  GGGACACGACTGGACATTCAA 321

```

RESULT 2 US-10-325-694-141

```

; Sequence 141, Application US/10325694
; Publication No. US20030148463A1
; GENERAL INFORMATION:
; APPLICANT: KUPER, PETER
; APPLICANT: RAUM, TOBIAS
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
; TITLE OF INVENTION: RECEPTORS AND USES THEREOF
; FILE REFERENCE: 38164000
; CURRENT APPLICATION NUMBER: US/10/325,694
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/09/403,107
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 141
; LENGTH: 321
; TYPE: DNA
; ORGANISM: HUMAN
US-10-325-694-141

```

Query Match 79.6%; Score 255.4; DB 15; Length 321;
Best Local Similarity 87.2%; Pred. No. 2.2e-78;
Matches 280; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

```

QY      1  GAGCTCCAGATGACCCAGTCTCCATCCTCCTGCTGTCATCTGTAGGAGACAGAGTCACC 60
Db      1  GAGCTCCAGATGACCCAGTCTCCATCCTCCTGCTGTCATCTGTAGGAGACAGAGTCACC 60
QY      61  ATCACTTCCGGGCAAGTCAAGAGCATTAGCAGCTATTAAATTGGTATCGAGAAACCA 120
Db      61  ATCACTTCCGGGCAAGTCAAGAGCATTAGCAGCTATTAAATTGGTATCGAGAAACCA 120
QY      121  GGACAGCTCTCTAAGCTGCTCATTTTACTGGGCACTTACCCGGGAATCCGGGCTCCCTGAC 180
Db      121  GGACAGCTCTCTAAGCTGCTCATTTTACTGGGCACTTACCCGGGAATCCGGGCTCCCTGAC 180
QY      181  CGATTTCAGCGGAGTGAATCTGGGACAAATTACACTCTGCACCTAGCAGCCT 240
Db      181  CGATTTCAGCGGAGTGAATCTGGGACAAATTACACTCTGCACCTAGCAGCCT 240
QY      241  GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCGATCACTTGGCCAA 300
Db      241  GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCGATCACTTGGCCAA 300
QY      301  GGGACACGACTGGACATTCAA 321
Db      301  GGGACACGACTGGACATTCAA 321

```

RESULT 3
US-10-344-514-7
; Sequence 7, Application US/10344514
; Publication No. US20040120951A1
; GENERAL INFORMATION:
; APPLICANT: NAKASHIMA, Toshihiro et al.

```

; TITLE OF INVENTION: HUMAN ANTI-FACTOR VIII ANTIBODY
; FILE REFERENCE: 0020-511P
; CURRENT APPLICATION NUMBER: US/10/344,514
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: JP 2001-177640
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 7
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-344-514-7

```

Query Match 76.6%; Score 245.8; DB 17; Length 324;
Best Local Similarity 85.4%; Pred. No. 4.9e-75;
Matches 274; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

```

QY      1  GAGCTCCAGATGACCCAGTCTCCATCCTCCTGCTGTCATCTGTAGGAGACAGAGTCACC 60
Db      1  GACATCCAGTTGACCCAGTCTCCATCCTCCTGCTGTCATCTGTAGGAGACAGAGTCACC 60
QY      61  ATCACTTCCGGGCAAGTCAAGAGCATTAGCAGCTATTAAATTGGTATCGAGAAACCA 120
Db      61  ATCACTTCCGGGCAAGTCAAGAGCATTAGCAGCTATTAAATTGGTATCGAGAAACCA 120
QY      121  GGACAGCTCTCTAAGCTGCTCATTTTACTGGGCACTTACCCGGGAATCCGGGCTCCCTGAC 180
Db      121  GGGAAAGCCCCAGTCTCTGATCTGCTGATCTGATCTGCAAAAGTGGGTCCCATCA 180
QY      181  CGATTTCAGCGGAGTGAATCTGGGACAAATTACACTCTGCACCTAGCAGCCT 240
Db      181  AGTTTCAGTGGAGTGAATCTGGGACAAATTACACTCTGCACCTAGCAGCCT 240
QY      241  GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCGATCACTTGGCCAA 300
Db      241  GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCGATCACTTGGCCAA 300
QY      301  GGGACACGACTGGACATTCAA 321
Db      301  GGGACACGACTGGACATTCAA 321

```

```

RESULT 4
US-10-344-514-8
; Sequence 8, Application US/10344514
; Publication No. US20040120951A1
; GENERAL INFORMATION:
; APPLICANT: NAKASHIMA, Toshihiro et al.
; TITLE OF INVENTION: HUMAN ANTI-FACTOR VIII ANTIBODY
; FILE REFERENCE: 0020-511P
; CURRENT APPLICATION NUMBER: US/10/344,514
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: JP 2001-177640
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 8
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(324)
US-10-344-514-8

```

Query Match 76.6%; Score 245.8; DB 17; Length 324;
Best Local Similarity 85.4%; Pred. No. 4.9e-75;
Matches 274; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

```

QY      1  GAGCTCCAGATGACCCAGTCTCCATCCTCCTGCTGTCATCTGTAGGAGACAGAGTCACC 60
Db      1  GACATCCAGTTGACCCAGTCTCCATCCTCCTGCTGTCATCTGTAGGAGACAGAGTCACC 60
QY      61  ATCACTTCCGGGCAAGTCAAGAGCATTAGCAGCTATTAAATTGGTATCGAGAAACCA 120

```

```
Db 61 ATCACTGCGGCGGAGTAGAGCATTAAGCATTAATTGGATACAGCAAAACA 120
Qy 121 GGAACAGCCTCTTAAGTGTCTCATTTAATCTGGGATCTACCCGGGAATCCGGGGTCCCTGAC 180
Db 121 GGGAAAGCCCCCTAAGCTCTGATCTATGCTGATGCTAGTTGGAAAGTGGGGGCCATCA 180
Qy 181 CATTTCAGGGGAGTAATCTGGGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
Db 181 AGGTTCAGTGGGAGTGTGAGGAGATTTCACTTCACTCAATCCATGAGAGTCTGCAACCT 240
Qy 241 GAAAGATTTGCTACTTCTTTGTCACAGTCTGACAGTTTGGCCGATCACTTCCGCA 300
Db 241 GAAAGATTTGCTACTTCTTACTACTGTCACAGAGTTAAGTACCCGATCACTTCCGCA 300
Qy 301 GGGACACGACTGGACATTCAA 321
Db 301 GGGACACGACTGGAGATTAA 321
```

RESULT 5

```
US-09-848-798-106
; Sequence 106, Application US/09848798
; Publication No. US20030040605A1
```

```
GENERAL INFORMATION:
```

```
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
```

```
FILE REFERENCE: 09596-4202
```

```
CURRENT APPLICATION NUMBER: US/09/848,798
```

```
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
```

```
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
```

```
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
```

```
NUMBER OF SEQ ID NOS: 224
```

```
SOFTWARE: PatentIn Ver. 2.0
```

```
SEQ ID NO 106
```

```
LENGTH: 321
```

```
TYPE: DNA
```

```
ORGANISM: Homo sapiens
```

```
FEATURE:
```

```
OTHER INFORMATION: anti-Rh(D) chain 106
```

```
Query Match 75.0%; Score 240.8; DB 10; Length 321;
```

```
Best Local Similarity 85.1%; Pred. No. 2.7e-73;
```

```
Matches 269; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
```

```
Qy 6 CCAAGTAGACCCAGTCTCCATCTCCCTGCTGCTGATCTGTAAGAGACAGAGTCAACCATC 65
Db 3 CGAGCTCACCCAGTCTCCATCTCCCTGCTGCTGATCTGTAAGAGAGAGTCAACCATC 62
Qy 66 TTGCGGGGAGAGTCAAGAGATTAGAGTATTAATTAATTAATTAATTAATTAATTAATTAAT 125
Db 63 TTGCGGGGAGAGTCAAGAGATTAGAGTATTAATTAATTAATTAATTAATTAATTAATTAAT 122
Qy 126 GCTCTTAAGTCTGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 185
Db 123 AGCCCTTAAGTCTGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 182
Qy 186 CAGCGGAGAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 245
Db 183 CAGTGCAGAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 242
Qy 246 TTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCCGATCACTTCCGCAAGGAG 305
Db 243 TTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCCGATCACTTCCGCAAGGAG 302
Qy 306 ACGACTGACATTCAA 321
Db 303 ACGACTGAGATTAA 318
```

RESULT 6

```
US-10-703-714-11
; Sequence 11, Application US/10703714
; Publication No. US20040170630A1
```

```
GENERAL INFORMATION:
```

```
APPLICANT: Huang, Haichun
```

```
APPLICANT: Holmes, Steven
```

```
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HEPARANASE
```

```
FILE REFERENCE: MX1-294
```

```
CURRENT APPLICATION NUMBER: US/10/703,714
```

```
PRIOR APPLICATION NUMBER: 60/424803
```

```
PRIOR FILING DATE: 2002-11-07
```

```
NUMBER OF SEQ ID NOS: 64
```

```
SOFTWARE: FastSeq for Windows Version 4.0
```

```
SEQ ID NO 11
```

```
LENGTH: 321
```

```
TYPE: DNA
```

```
ORGANISM: Homo sapiens
```

```
FEATURE:
```

```
NAME/KEY: CDS
```

```
LOCATION: (1)...(321)
```

```
US-10-703-714-11
```

```
Query Match 74.8%; Score 240.2; DB 17; Length 321;
```

```
Best Local Similarity 84.9%; Pred. No. 4.3e-73;
```

```
Matches 269; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
```

```
Qy 5 TCAGATGACCCAGTCTCCATCTCCCTGCTGCTGATCTGTAAGAGAGAGTCAACCATC 64
Db 5 TCAGATGACCCAGTCTCCATCTCCCTGCTGCTGATCTGTAAGAGAGAGTCAACCATC 64
Qy 65 TTGCGGGGAGAGTCAAGAGATTAGAGTATTAATTAATTAATTAATTAATTAATTAATTAAT 124
Db 65 TTGCGGGGAGAGTCAAGAGATTAGAGTATTAATTAATTAATTAATTAATTAATTAATTAAT 124
Qy 125 AGCTCTTAAGTCTGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 184
Db 125 AGCTCTTAAGTCTGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 184
Qy 185 TCAGGCGGAGAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 244
Db 185 TCAGGCGGAGAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 244
Qy 245 ATTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGGCCGATCACTTCCGCAAGGAG 304
Db 245 ATTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGGCCGATCACTTCCGCAAGGAG 304
Qy 305 CACGACTGGACATTCAA 321
Db 305 CACGACTGGAGATTAA 321
```

RESULT 7

```
US-10-703-714-19
; Sequence 19, Application US/10703714
; Publication No. US20040170630A1
```

```
GENERAL INFORMATION:
```

```
APPLICANT: Huang, Haichun
```

```
APPLICANT: Holmes, Steven
```

```
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HEPARANASE
```

```
FILE REFERENCE: MX1-294
```

```
CURRENT APPLICATION NUMBER: US/10/703,714
```

```
PRIOR APPLICATION NUMBER: 60/424803
```

```
PRIOR FILING DATE: 2002-11-07
```

```
NUMBER OF SEQ ID NOS: 64
```

```
SOFTWARE: FastSeq for Windows Version 4.0
```

```
SEQ ID NO 19
```

```
LENGTH: 321
```

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(321)
US-10-703-714-19

Query Match 74.8%; Score 240.2; DB 17; Length 321;
Best Local Similarity 84.9%; Pred. No. 4.3e-73;
Matches 269; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 5 TCAGATGACCCAGTCTCCCTCTGTCATCTGTAGAGACAGAGTCAACCATCA 64
DB 5 TCAGATGACCCAGTCTCCCTCTGTCATCTGTAGAGACAGAGTCAACCATCA 64
QY 65 CTGGCCGGGCAAGTCAGAGCATTAGCAGCTATTAAATGGTATCAAGCAAAACAGGAC 124
DB 65 CTGGCCGGGCAAGTCAGAGCATTAGCAGCTATTAAATGGTATCAAGCAAAACAGGAC 124
QY 125 AGCCTCTAGCTCTGATCTGATGATGCTCCAGTTTGAAGTGGGTCCCTGACCGAT 184
DB 125 AGCCTCTAGCTCTGATCTGATGATGCTCCAGTTTGAAGTGGGTCCCTGACCGAT 184
QY 185 TCAGCCGACAGTGAATCTGGGACAATTAATCACTCTCAACATCAGACCTGACGCTGAAG 244
DB 185 TCAGCCGACAGTGAATCTGGGACAATTAATCACTCTCAACATCAGACCTGACGCTGAAG 244
QY 245 ATTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTCCGATCACTTCCGCAAGGGA 304
DB 245 ATTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTCCGATCACTTCCGCAAGGGA 304
QY 305 CACGACTGACATTCAA 321
DB 305 CACGACTGACATTCAA 321

RESULT 8
US-10-309-762-215
Sequence 215, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
FILE REFERENCE: AGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 215
LENGTH: 322
TYPE: DNA
ORGANISM: Homo sapiens
US-10-309-762-215

Query Match 74.6%; Score 239.4; DB 16; Length 322;
Best Local Similarity 84.1%; Pred. No. 8.3e-73;
Matches 270; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
QY 1 GAGCTCCAGATGACCCAGTCTCCCTCTGTCATCTGTAGAGACAGAGTCAAC 60
DB 1 GAGCTCCAGATGACCCAGTCTCCCTCTGTCATCTGTAGAGACAGAGTCAAC 60
QY 61 ATCACTTGGCCGACAGTGAAGATTAAGATTAATGGTATCAGAGAAACA 120
DB 61 ATCACTTGGCCGACAGTGAAGATTAAGATTAATGGTATCAGAGAAACA 120
QY 121 GGACAGCTCTTAAGCTGTCTATTACTGGGCACTTACCCGGGAATCCGGGGTCCCTGAC 180

DB 121 GGGAAAGCCCTTACTCTCTGATCTATGCTGATCTCAAGTTGGAAAGTGGGTCCCATCA 180
QY 181 CGATTCAAGCGGAGTGAATCTGGGACAATTAATCACTCTCAACATCAGAGCTGACGCT 240
DB 181 AGTTCAAGCGGAGTGAATCTGGGACAATTAATCACTCTCAACATCAGAGCTGACGCT 240
QY 241 GAAGATTTTGTCTACTTCTTGTCAACAGTGTGACAGTTTCCGATCACTTCCGCA 300
DB 241 GAAGATTTTGTCTACTTCTTGTCAACAGTGTGACAGTTTCCGATCACTTCCGCA 300
QY 301 GGGACAGCACTGACATTCAA 321
DB 301 GGGACAGCACTGACATTCAA 321

RESULT 9
US-10-309-762-228
Sequence 228, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
FILE REFERENCE: AGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 228
LENGTH: 322
TYPE: DNA
ORGANISM: Homo sapiens
US-10-309-762-228

Query Match 74.6%; Score 239.4; DB 16; Length 322;
Best Local Similarity 84.1%; Pred. No. 8.3e-73;
Matches 270; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCCTCTGTCATCTGTAGAGACAGAGTCAAC 60
DB 1 GAGCTCCAGATGACCCAGTCTCCCTCTGTCATCTGTAGAGACAGAGTCAAC 60
QY 61 ATCACTTGGCCGACAGTGAAGATTAAGATTAATGGTATCAGAGAAACA 120
DB 61 ATCACTTGGCCGACAGTGAAGATTAAGATTAATGGTATCAGAGAAACA 120
QY 121 GGACAGCTCTTAAGCTGTCTATTACTGGGCACTTACCCGGGAATCCGGGGTCCCTGAC 180
DB 121 GGACAGCTCTTAAGCTGTCTATTACTGGGCACTTACCCGGGAATCCGGGGTCCCTGAC 180
QY 181 CGATTCAAGCGGAGTGAATCTGGGACAATTAATCACTCTCAACATCAGAGCTGACGCT 240
DB 181 CGATTCAAGCGGAGTGAATCTGGGACAATTAATCACTCTCAACATCAGAGCTGACGCT 240
QY 241 GAAGATTTTGTCTACTTCTTGTCAACAGTGTGACAGTTTCCGATCACTTCCGCA 300
DB 241 GAAGATTTTGTCTACTTCTTGTCAACAGTGTGACAGTTTCCGATCACTTCCGCA 300
QY 301 GGGACAGCACTGACATTCAA 321
DB 301 GGGACAGCACTGACATTCAA 321
RESULT 10
US-10-309-762-213
Sequence 213, Application US/10309762
Publication No. US20040018198A1

```
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Poltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IX
FILE REFERENCE: ABGENIX 027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 213
LENGTH: 322
TYPE: DNA
ORGANISM: Homo sapiens
US-10-309-762-213
```

```
Query Match      73.6%; Score 236.2; DB 16; Length 322;
Best Local Similarity 83.5%; Pred. No. 1.1e-71;
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
```

```
QY 1 GAGCTCCAGATGACCCAGTCTCCATCCCTGCTGCACTGTAGAGACAGAGTCACC 60
    |||||||
DB 1 GACATCCAGATGACCCAGTCTCCATCCCTGCTGCACTGTAGAGACAGAGTCACC 60

QY 61 ATCACTTGGCCGGGCAAGTCAAGACATTAGAGCATTTAATGGTATCAGCAAAACCA 120
    |||||||
DB 61 ATCACTTGGCCGGGCAAGTCAAGACATTAGAGCATTTAATGGTATCAGCAAAACCA 120

QY 121 GGAAGATTTGGCTACTTACTTTGTCAACAGCTGACAGTTGGCGATCACTTCGGCCAA 300
    |||||||
DB 121 GGAAGATTTGGCTACTTACTTTGTCAACAGCTGACAGTTGGCGATCACTTCGGCCAA 300

QY 181 CGATTGAGGGGCGAGTGAATCTGGGACAAATTACACTCTCCATCCAGCAGCCCT 240
    |||||||
DB 181 AGTTGAGGGGCGAGTGAATCTGGGACAAATTACACTCTCCATCCAGCAGCCCT 240

QY 241 GAAGATTTGGCTACTTACTTTGTCAACAGCTGACAGTTGGCGATCACTTCGGCCAA 300
    |||||||
DB 241 GAAGATTTGGCTACTTACTTTGTCAACAGCTGACAGTTGGCGATCACTTCGGCCAA 300

QY 301 GGGACACGACTGGACATTCAA 321
    |||||||
DB 301 GGGACACGACTGGACATTCAA 321
```

```
RESULT 11
US-10-309-762-238
Sequence 238, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Poltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IX
FILE REFERENCE: ABGENIX 027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 238
LENGTH: 322
TYPE: DNA
ORGANISM: Homo sapiens
US-10-309-762-238
```

```
Query Match      73.6%; Score 236.2; DB 16; Length 322;
Best Local Similarity 83.5%; Pred. No. 1.1e-71;
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCCCTGCTGCACTGTAGAGACAGAGTCACC 60
    |||||||
DB 1 GACATCCAGATGACCCAGTCTCCATCCCTGCTGCACTGTAGAGACAGAGTCACC 60

QY 61 ATCACTTGGCCGGGCAAGTCAAGACATTAGAGCATTTAATGGTATCAGCAAAACCA 120
    |||||||
DB 61 ATCACTTGGCCGGGCAAGTCAAGACATTAGAGCATTTAATGGTATCAGCAAAACCA 120

QY 121 GGAAGATTTGGCTACTTACTTTGTCAACAGCTGACAGTTGGCGATCACTTCGGCCAA 300
    |||||||
DB 121 GGAAGATTTGGCTACTTACTTTGTCAACAGCTGACAGTTGGCGATCACTTCGGCCAA 300

QY 181 CGATTGAGGGGCGAGTGAATCTGGGACAAATTACACTCTCCATCCAGCAGCCCT 240
    |||||||
DB 181 AGTTGAGGGGCGAGTGAATCTGGGACAAATTACACTCTCCATCCAGCAGCCCT 240

QY 241 GAAGATTTGGCTACTTACTTTGTCAACAGCTGACAGTTGGCGATCACTTCGGCCAA 300
    |||||||
DB 241 GAAGATTTGGCTACTTACTTTGTCAACAGCTGACAGTTGGCGATCACTTCGGCCAA 300

QY 301 GGGACACGACTGGACATTCAA 321
    |||||||
DB 301 GGGACACGACTGGACATTCAA 321
```

```
RESULT 12
US-10-264-049-121
Sequence 121, Application US/10264049
Publication No. US2004000579A1
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA133P1
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 121
LENGTH: 1106
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (302)..(302)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: misc.feature
LOCATION: (424)..(424)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1035)..(1039)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1084)..(1084)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1103)..(1103)
OTHER INFORMATION: n equals a,t,g, or c
US-10-264-049-121
```

```
Query Match      73.2%; Score 235; DB 16; Length 1106;
Best Local Similarity 81.6%; Pred. No. 4.6e-71;
```


Matches 262; Conservative 6; Mismatches 53; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCTGTCTGATCTGTAGAGACAGAGTACC 60
|||
Db 145 GACATCCAGATGACCCAGTCTCCATCTCTGTCTGATCTGTAGAGACAGAGTACC 204
61 ATCACTTGGCCGGCAGTACAGAGCATTTAGAGTATTTAAATTTGGATCAGAGAAACA 120
|||
Db 205 ATCACTTGGCCGGCAGTACAGAGCATTTAGAGTATTTAAATTTGGATCAGAGAAACA 264
121 GAGACGCTCTTAAGCTGTCTATTTACTGGGCATCTACCCGGGAATCCGGGTCCCTGAC 180
|||
Db 265 GGGAAAGCCCTTAAGCTGTCTATTTACTGGGCATCTACCCGGGAATCCGGGTCCCTGAC 324
QY 181 CGATTGAGGGGAGTGAATCTGGGACAAATTACACTCTCAACATCAGACGCTGACGCT 240
|||
Db 325 AGGTCAGTGGCAGTGAATCTGGGACAAATTACACTCTCAACATCAGACGCTGACGCT 384
QY 241 GAAGATTTTGTACTACTTTTGTCAACAGTCTGACAGTGTGCGATCCTTCCGGCCAA 300
|||
Db 385 GAAGATTTTGTCAACTTAATCTGTCAACAGTATGATTAATNTCCCTCTCACTTTCGGCSRA 444
QY 301 GGGACAGACTGGACATTCAA 321
|||
Db 445 GGGACCAAGGTGAGARATCAA 465

RESULT 13
US-10-203-754A-60
; Sequence 60, Application US/10203754A
; Publication No. US20030157132A1
; GENERAL INFORMATION:
; APPLICANT: ITAMI, Seima
; APPLICANT: SEKI, Makoto
; APPLICANT: MATSURA, Yoshiharu
; APPLICANT: SHIBUI, Tetsuro
; APPLICANT: YOTSUMOTO, Yoshihisa
; APPLICANT: MIYAMURA, Tatsuo
; TITLE OF INVENTION: Therapeutic Agent for Hepatitis C
; FILE REFERENCE: P22257
; CURRENT APPLICATION NUMBER: US/10/203,754A
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/JP01/00967
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-203-754A-60

Query Match 72.1%; Score 231.4; DB 15; Length 333;
Best Local Similarity 82.6%; Pred. No. 5.2e-70;
Matches 265; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Db 241 GAAGATTTTGTCAACTTACTGTGTCAACAGATTAAGATCCCTCTCACTTTCGGCCGA 300
|||
QY 301 GGGACAGACTGGACATTCAA 321
|||
Db 301 GGGACCAAGGTGAGATCAA 321

RESULT 14
US-09-192-854-1
; Sequence 1, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; PRIOR FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-192-854-1

Query Match 72.1%; Score 231.4; DB 9; Length 720;
Best Local Similarity 82.6%; Pred. No. 7e-70;
Matches 265; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCTGTCTGATCTGTAGAGACAGAGTACC 60
|||
Db 397 GACATCCAGATGACCCAGTCTCCATCTCTGTCTGATCTGTAGAGACAGAGTACC 456
61 ATCACTTGGCCGGCAGTACAGAGCATTTAGAGTATTTAAATTTGGATCAGAGAAACA 120
|||
Db 457 ATCACTTGGCCGGCAGTACAGAGCATTTAGAGTATTTAAATTTGGATCAGAGAAACA 516
121 GAGACGCTCTTAAGCTGTCTATTTACTGGGCATCTACCCGGGAATCCGGGTCCCTGAC 180
|||
Db 517 GGGAAAGCCCTTAAGCTGTCTATTTACTGGGCATCTACCCGGGAATCCGGGTCCCTGAC 576
QY 181 CGATTGAGGGGAGTGAATCTGGGACAAATTACACTCTCAACATCAGACGCTGACGCT 240
|||
Db 577 AGGTCAGTGGCAGTGAATCTGGGACAAATTACACTCTCAACATCAGACGCTGACGCT 636
QY 241 GAAGATTTTGTACTACTTTTGTCAACAGTCTGACAGTGTGCGATCCTTCCGGCCAA 300
|||
Db 637 GAAGATTTTGTCAACTTACTGTGTCAACAGATTAAGATCCCTCTCACTTTCGGCCGA 696
QY 301 GGGACAGACTGGACATTCAA 321
|||
Db 697 GGGACCAAGGTGAGATCAA 717

RESULT 15
US-09-968-561A-1
; Sequence 1, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phase Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13

;; PRIOR APPLICATION NUMBER: US 60/066,729
;; PRIOR FILING DATE: 1997-11-21
;; PRIOR APPLICATION NUMBER: PCT/GB98/03135
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: US 09/511,939
;; PRIOR FILING DATE: 2000-02-24
;; NUMBER OF SEQ ID NOS: 350
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 1
;; LENGTH: 720
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-968-561A-1

Query Match 72.1%; Score 231.4; DB 9; Length 720;
Best Local Similarity 82.6%; Pred. No. 7e-70;
Matches 265; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCATCTCCCTGTCTGATCTGTAGAGACAGAGTCACC 60
DB 397 GACATCCAGATGACCCAGTCTCATCTCCCTGTCTGATCTGTAGAGACAGAGTCACC 456
QY 61 ATCACTTGCCTGGGCAAGTCAAGCATTAGCAGCTATTAAATTGATCAGAGAAACA 120
DB 457 ATCACTTGCCTGGGCAAGTCAAGCATTAGCAGCTATTAAATTGATCAGAGAAACA 516
QY 121 GGCAGCCTCTTAAAGTGTCTATTACTGGGCATCTACCCGGGAATCCGGGTCCTGAC 180
DB 517 GGGAAAGCCCTTAAGCTCTGATCTATGCTGATCCAGTTTGCAAGTGGGGTCCCATCA 576
QY 181 CGATTGAGGGGCGAGTAATCTGGGACAAATTACATCTCAGCATCAGAGCCTGCAAGCT 240
DB 577 AGGTTGAGTGGGAGTGAATCTGGGACAAATTACATCTCAGCATCAGAGCCTGCAAGCT 636
QY 241 GAAGATTTTGTCTACTTCTTTGTCAACAGTGTGACAGTTTGGCCGATCAGCTTGGCCAA 300
DB 637 GAAGATTTTGTCTACTTCTTTGTCAACAGTGTGACAGTTTGGCCGATCAGCTTGGCCAA 696
QY 301 GGGACACGACTGGACATTCAA 321
DB 697 GGGACCAAGGTGGAATCAAA 717

Search completed: December 7, 2004, 14:26:31
Job time : 275.899 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 06:11:35 ; Search time 1873.31 Seconds
(without alignments)
6244.126 Million cell updates/sec

Title: US-09-403-107-147

Perfect score: 321

Sequence: 1 gagctccagatgaccacgacgc.....ggacacgactggacattcaa 321

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_hlc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	238.4	74.3	353	2	AM404894 UT-HF-BLO
2	237.8	74.1	794	6	CB955875 AGENCOURT
3	236.2	73.6	621	4	BM171889 imagegc_3
4	236.2	73.6	748	6	CB957070 AGENCOURT
5	234.6	73.1	826	4	BG742662 602633264
6	233	72.6	709	6	CD690167 EST6680 h
7	233	72.6	781	6	CB985512 AGENCOURT
8	231.6	72.1	553	6	CD705041 EST21568
9	231.4	72.1	421	2	AM406227 UT-HF-BLO
10	231.4	72.1	422	2	AM407904 UT-HF-BLO
11	231.4	72.1	521	6	CD707755 EST24282
12	231.4	72.1	587	4	BG756289 602713607
13	231.4	72.1	624	6	CD690145 EST6668 h
14	230.6	71.8	570	4	BG536784 602566318
15	229.8	71.6	486	6	CD683960 EST480 hu
16	229.8	71.6	493	3	AM405753 UT-HF-BLO
17	229.8	71.6	797	6	CB987347 AGENCOURT
18	229.8	71.6	831	6	CB987031 AGENCOURT
19	228.2	71.1	525	6	CD705928 EST22455
20	228.2	71.1	708	6	CB956923 AGENCOURT
21	228.2	71.1	773	4	BM007845 603617528
22	227.4	70.8	339	1	AB107216 AB107216
23	227.4	70.8	499	6	CD685478 EST1998 h
24	226.6	70.6	487	2	AM405301 UT-HF-BLO

25	226.6	70.6	559	4	BG547768	BG547768 602575646
26	226.6	70.6	693	6	CD684441	CD684441 EST961 hu
27	226.6	70.6	754	6	CB986767	CB986767 AGENCOURT
28	226.6	70.6	785	6	CB955817	CB955817 AGENCOURT
29	226.6	70.6	864	4	BG548281	BG548281 602575248
30	226.6	70.6	923	5	BQ882857	BQ882857 AGENCOURT
31	226.4	70.5	740	6	CB987627	CB987627 AGENCOURT
32	226.4	70.5	756	6	CB984720	CB984720 AGENCOURT
33	225.8	70.3	608	2	AM404714	AM404714 UT-HF-BLO
34	225.8	70.3	921	2	BG341239	BG341239 602463904
35	225	70.1	391	2	AM404992	AM404992 UT-HF-BLO
36	225	70.1	460	2	AM405906	AM405906 UT-HF-BLO
37	225	70.1	510	6	CD694557	CD694557 EST11080
38	225	70.1	550	6	CD709957	CD709957 EST26484
39	225	70.1	566	6	AM406081	AM406081 UT-HF-BLO
40	225	70.1	695	6	CD683876	CD683876 EST136 hu
41	225	70.1	724	6	CB959008	CB959008 AGENCOURT
42	225	70.1	742	6	CB984723	CB984723 AGENCOURT
43	225	70.1	759	6	CB986444	CB986444 AGENCOURT
44	225	70.1	785	6	CB986976	CB986976 AGENCOURT
45	225	70.1	820	6	CB956240	CB956240 AGENCOURT

ALIGNMENTS

RESULT 1
AM404894 353 bp mRNA linear EST 16-FEB-2000
UT-HF-BLO-acn-f-07-0-UI-r1 NIH MGC_37 Homo sapiens CDNA clone
LOCUS IMAGE:3059844 5', mRNA sequence.

ACCESSION AM404894
VERSION AM404894.1 GI:6923951
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bdip/image/image.html
Seq primer: M13 Forward.

FEATURES

Location/Qualifiers
1..353
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3059844"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: pTR73-Pac; Site 1: NotI; Site 2: Eco RI; constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 74.3% Score 238.4; DB 2; Length 353;
Best Local Similarity 85.3%; Pred. No. 5.5e-66;

Matches 266; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCACTGTAGAGACAGAGTACC 60
 |||||
 Db 42 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCACTGTAGAGACAGAGTACC 101
 |||||
 QY 61 ATCACTTCCGGGCAAGTCAAGACATTAAGACATTAATTTGATACAGAGAACCA 120
 |||||
 Db 102 ATCACTTCCGGGCAAGTCAAGACATTAAGACATTAATTTGATACAGAGAACCA 161
 |||||
 QY 121 GAGACAGCTCTTAAGTGTCTCATTTTACTGGGCACTACCCGGGATCCGGGGTCCCTGAC 180
 |||||
 Db 162 GGGAAAGCCCTTAGGCTCTGATCTATGCTGCACTTCAGATTGGAGAGTGGGCTCCATCA 221
 |||||
 QY 181 CGATTGAGCGGAGTGAATCTGGAGCAATTAACCTTCACATCAGACAGCTTCAGACCT 240
 |||||
 Db 222 AGGTTCAGTGGCAGTGGATCTGGAGACAGATTTCACCTCAGCAGAGTCTGCAACT 281
 |||||
 QY 241 GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTGGCCGATCAGCTTGGGCCAA 300
 |||||
 Db 282 GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTGGCCGATCAGCTTGGGCCAA 341
 |||||
 QY 301 GGGACACGACTG 312
 |||||
 Db 342 GGGACACGACTG 353
 |||||

RESULT 2
 CB955875 794 bp mRNA linear EST 29-APR-2003
 LOCUS CB955875
 DEFINITION AGENCOURT 13779371 NIH_MGC_184 Homo sapiens cDNA clone
 IMAGE:30349554 5', mRNA sequence.

ACCESSION CB955875
 VERSION CB955875.1 GI:30211993
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 JOURNAL 1 (bases 1 to 794)
 COMMENT NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@pds-remail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: NDCM144 row: a column: 19
 High quality sequence stop: 520.
 Location/Qualifiers

FEATURES
 source 1..794
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30349554"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_1lb="NIH MGC 184"
 /note="Organ: Pooled-glandular; Vector: pDNR-LIB, Site 1:
 SfiI (ggccatctggcc); Site 2: SfiI (ggccgctcggcc);
 Library is oligo-dT primed and directionally cloned. cDNA
 was prepared from a glandular pool of tissues from thyroid,
 parathyroid, adrenal, cortex and pineal gland. 5' and 3'
 adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CACGGCCATTATGCGC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGGAGGCGGCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.38
 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

Query Match 74.1%; Score 237.8; DB 6; Length 794;
 Best Local Similarity 83.8%; Pred. No. 1.2e-65;
 Matches 269; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCACTGTAGAGACAGAGTACC 60
 |||||
 Db 94 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCACTGTAGAGACAGAGTACC 153
 |||||
 QY 61 ATCACTTCCGGGCAAGTCAAGACATTAAGACATTAATTTGATACAGAGAACCA 120
 |||||
 Db 154 ATCACTTCCGGGCAAGTCAAGACATTAAGACATTAATTTGATACAGAGAACCA 213
 |||||
 QY 121 GAGACAGCTCTTAAGTGTCTCATTTTACTGGGCACTACCCGGGATCCGGGGTCCCTGAC 180
 |||||
 Db 214 GGGAAAGCCCTTAGGCTCTGATCTATGCTGCACTTCAGATTGGAGAGTGGGCTCCATCA 273
 |||||
 QY 181 CGATTGAGCGGAGTGAATCTGGAGCAATTAACCTTCACATCAGACAGCTTCAGACCT 240
 |||||
 Db 274 AGGTTCAGTGGCAGTGGATCTGGAGACAGATTTCACCTCAGCAGAGTCTGCAACT 333
 |||||
 QY 241 GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTGGCCGATCAGCTTGGGCCAA 300
 |||||
 Db 334 GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTGGCCGATCAGCTTGGGCCAA 393
 |||||
 QY 301 GGGACACGACTGAGACTTCAA 321
 |||||
 Db 394 GGGACACGACTGAGACTTCAA 414
 |||||

RESULT 3
 BM171889 621 bp mRNA linear EST 04-DEC-2001
 LOCUS BM171889
 DEFINITION image3 3 2001/smm27bdf41.x1 NIH_MGC_77 Homo sapiens cDNA clone
 IMAGE:4690577 5', mRNA sequence.

ACCESSION BM171889
 VERSION BM171889.1 GI:17311452
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 JOURNAL 1 (bases 1 to 621)
 COMMENT NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (2001)
 Contact: Prange CK
 The I.M.A.G.E. Consortium
 Lawrence Livermore National Laboratory
 Livermore, CA, USA
 Email: help@image.llnl.gov
 This read has been verified (found to hit its original self in the
 correct orientation), as part of the I.M.A.G.E. Consortium quality
 control effort. High quality sequence is defined as having 100 or
 more base pairs with a phred quality value of 20 or greater, where
 a sliding window of 4 base pairs with a phred quality value of 15
 or greater marks the beginning and end of the sequence. For
 information on obtaining this clone, please contact
 info@image.llnl.gov.
 Plate: LNCM1509 row: c column: 6
 Seq primer: -21m13
 High quality sequence stop: 621.
 Location/Qualifiers

FEATURES
 source 1..621
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"

```
/clone="IMAGE:4690877"  
/lab host="DH10B (T1 phage-resistant)"  
/note="Organ: Lung; Vector: pDNR-LIB (Clontech); Site_1:  
5'f1 (ggcgccctggcc); Site_2: 5'f1 (ggccatcggcc); 5' and  
3' adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCGCGAGCGCCGACATG-dr (30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.9  
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH_MGC Library."
```

ORIGIN

```
Query Match 73.6%; Score 236.2; DB 4; Length 621;  
Best Local Similarity 83.5%; Pred. No. 3.5e-65;  
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
```

```
1 GAGCTCCAGATGACCCAGTCTCATCTCCCTGTCGATCTGTAGAGACAGATCACC 60  
|||  
90 GATTGCCAGATGACCCAGTCTCATCTCCCTGTCGATCTGTAGAGACAGATCACC 149  
|||  
61 ATCACTTGCCTGAGCAAGTCAAGACATTAGCAGCTATTAAATGGTATCAGAGAAACCA 120  
|||  
150 GCCACTTGGCGGGCAAGTCAAGACATTAAATTTAATGGTATCAGAGAAACCA 209  
|||  
121 GGCACGCTCTTAAGTCTCATCTGCTGAGCACTACCGGGAATCCGGGTCCTGAC 180  
|||  
210 GGGCAAGCCCTTAAGTCTCATCTGATTTATGGTCATCCACTTGGCAAGTGGGGTCCCATCA 269  
|||  
181 CGATTAGCGGCGAGTGAATGTGGACAAATTACATCTCCATCCATCAGACCTCGACCT 240  
|||  
270 AGGTTAGTGGCGAGTGAATGTGGACAAATTACATCTCCATCCATCAGACCTCGACCT 329  
|||  
241 GAAGATTTGCTACTTACTTTGTCAACAGTCTGACAGTGGCGATCACTTCGAGCA 300  
|||  
330 GAAGATTTGCTACTTACTTTGTCAACAGTCTGACAGTGGCGATCACTTCGAGCA 389  
|||  
QY 301 GGGACACGACTGGACATTCAA 321  
|||  
Db 390 GGGACACGACTGGACATTCAA 410  
|||
```

```
RESULT 4 748 bp mRNA linear EST 29-APR-2003  
LOCUS CB957070  
DEFINITION AGENCOURT 13777897 NIH MGC 184 Homo sapiens cDNA clone  
IMAGE:30350034 5', mRNA sequence.  
CB957070  
CB957070.1 GI:30213187
```

```
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT
```

```
Human sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 748)  
NIH-MGC http://mgs.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: NDCM45 row: e column: 19  
High quality sequence stop: 507.  
Location/Qualifiers  
1..748  
source
```

```
/organism="Homo sapiens"  
/mol_type="mRNA"  
/db_xref="taxon:9606"  
/clone="IMAGE:30350034"  
/lab host="DH10B (T1 phage-resistant)"  
/note="Organ: Pooled-glandular; Vector: pDNR-LIB; Site_1:  
5'f1 (ggcgccctggcc); Site_2: 5'f1 (ggcgccctggcc);  
Library is oligo-dr primed and directionally cloned. cDNA  
was prepared from a glandular pool of tissues from thyroid,  
parathyroid, adrenal, cortex and pineal gland. 5' and 3'  
adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCGCGAGCGCCGACATG-dr (30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.38  
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH_MGC Library."
```

ORIGIN

```
Query Match 73.6%; Score 236.2; DB 6; Length 748;  
Best Local Similarity 83.5%; Pred. No. 3.8e-65;  
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
```

```
1 GAGCTCCAGATGACCCAGTCTCATCTCCCTGTCGATCTGTAGAGACAGATCACC 60  
|||  
89 GACATCCAGATGACCCAGTCTCATCTCCCTGTCGATCTGTAGAGACAGATCACC 148  
|||  
61 ATCACTTGCCTGAGCAAGTCAAGACATTAGCAGCTATTAAATGGTATCAGAGAAACCA 120  
|||  
149 ATCACTTGCCTGAGCAAGTCAAGACATTAGCAGCTATTAAATGGTATCAGAGAAACCA 208  
|||  
121 GGCACGCTCTTAAGTCTCATCTGCTGAGCACTACCGGGAATCCGGGTCCTGAC 180  
|||  
209 GGGGAAGCCCTTAAGTCTCATCTGATTTATGGTCATCCACTTGGCAAGTGGGGTCCCATCA 268  
|||  
181 CGATTAGCGGCGAGTGAATGTGGACAAATTACATCTCCATCCATCAGACCTCGACCT 240  
|||  
269 AGGTTAGTGGCGAGTGAATGTGGACAAATTACATCTCCATCCATCAGACCTCGACCT 328  
|||  
241 GAAGATTTGCTACTTACTTTGTCAACAGTCTGACAGTGGCGATCACTTCGAGCA 300  
|||  
329 GATGATTTGCTACTTACTTTGTCAACAGTCTGACAGTGGCGATCACTTCGAGCA 388  
|||  
QY 301 GGGACACGACTGGACATTCAA 321  
|||  
Db 389 GGGACACGACTGGACATTCAA 409  
|||
```

```
RESULT 5 826 bp mRNA linear EST 15-MAY-2001  
LOCUS BG742662  
DEFINITION 602633264F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4778726 5',  
mRNA sequence.  
BG742662  
BG742662.1 GI:14053315
```

```
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT
```

```
Human sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 826)  
NIH-MGC http://mgs.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: James Cleaver, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA  
Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be
```

found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLNL0634 row: 0 column: 15
 High quality sequence stop: 824.
 Location/Qualifiers

FEATURES

1..826

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4778726"

/lab_host="DH10B (TI phage-resistant)"

/clone_lib="NCI CGAP Skn3"

/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI CGAP Library."

ORIGIN

Query Match 73.1%; Score 234.6; DB 4; Length 826;

Best Local Similarity 83.2%; Pred. No. 1.3e-64;

Matches 267; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCGATCTGTAGAGACAGAGTACC 60
 |||
 55 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCGATCTGTAGAGACAGAGTACC 114
 |||
 61 ATCACTTCCGCGGAGAGTCAAGAGCTTGAAGTATTAATTGTTATAGACAGAAACA 120
 |||
 115 ATCACTTCCGCGGAGAGTCAAGAGCTTGAAGTATTAATTGTTATAGACAGAAACA 174
 |||
 121 GGAACACCTCTTCAAGCTGCTCATTTTCTGGGATCTAACCCGGGAATCCGGGGTCCCTGAC 180
 |||
 175 GGGAAAGCCCCCTTAACCTCTGATTCATGTCATCCAGTCTGAGAGTGGGGTCCCATCA 234
 |||
 181 CGATTACGGGCGAGTAAATCTGGGACAAATTACACTCTACATCAGACAGCTGACGCT 240
 |||
 235 AGGTTCAAGTGGAGTGGATCTGGGACAGATTTCACCTCACTACATCAGTAGTCTGCAACT 294
 |||
 241 GAAGATTTTGTCTACTTCTTTGTCAACAGTCTGACAGTTTGGCCGATCAGCTTGGCCAA 300
 |||
 295 GAAGATTTTGTCTACTTCTTTCTCAACAGGTTTACAGTACGAGCTTACCTTGGCCAA 354
 |||
 301 GGGACACGACTGGACATTTCA 321
 |||
 355 GGGACACGACTGGACATTTAA 375
 |||

RESULT 6
 CD690167 709 bp mRNA linear EST 25-JUN-2003

DEFINITION EST6890 human nasopharynx Homo sapiens cDNA, mRNA sequence.

ACCESSION CD690167.1 GI:32210659

VERSION

KEYWORDS

SOURCE EST.

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 709)

Liu X.-Q., Zhou Y., Zhang L.-J., Xu H., Chen H.-K., Pan Z.-G. and

Zeng Y.-X.

Transcriptional Gene Expression Profile of Human Nasopharynx

Unpublished (2003)

CONTACT: Yixin Zeng

Cancer Center

Sun Yat-sen University

651 Dongfeng Road East, Guangzhou 510060, China

Tel: 86-1380-9770-743

Fax: 86-20-8775-4506

Email: yxzeng@zsums.edu.cn.

Location/Qualifiers

1..709

/organism="Homo sapiens"

/mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="human nasopharynx"
 /note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Query Match 72.6%; Score 233; DB 6; Length 709;

Best Local Similarity 82.9%; Pred. No. 4.1e-64;

Matches 266; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCGATCTGTAGAGACAGAGTACC 60
 |||
 123 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCGATCTGTAGAGACAGAGTACC 182
 |||
 61 ATCACTTCCGCGGAGAGTCAAGAGCTTGAAGTATTAATTGTTATAGACAGAAACA 120
 |||
 183 ATCACTTCCGCGGAGAGTCAAGAGCTTGAAGTATTAATTGTTATAGACAGAAACA 242
 |||
 121 GGAACACCTCTTCAAGCTGCTCATTTTCTGGGATCTAACCCGGGAATCCGGGGTCCCTGAC 180
 |||
 243 GGGAAAGCCCCCTTAACCTCTGATTCATGTCATCCAGTCTGAGAGTGGGGTCCCATCA 302
 |||
 181 CGATTACGGGCGAGTAAATCTGGGACAAATTACACTCTACATCAGACAGCTGACGCT 240
 |||
 303 AGGTTCAAGTGGAGTGGATCTGGGACAGATTTCATCCATCAGACAGCTTGGCCAA 362
 |||
 241 GAAGATTTTGTCTACTTCTTTGTCAACAGTCTGACAGTTTGGCCGATCAGCTTGGCCAA 300
 |||
 363 GAAGATTTTGTCTACTTCTTTCTCAACAGGTTTACAGTACGAGCTTACCTTGGCCAA 422
 |||
 301 GGGACACGACTGGACATTTCA 321
 |||
 423 GGGACACGACTGGACATTTAA 443
 |||

RESULT 7
 CB985512 781 bp mRNA linear EST 01-MAY-2003

DEFINITION AGENCOURT 13672145 NIH MGC 184 Homo sapiens cDNA clone

IMAGE:30327573 5', mRNA sequence.

ACCESSION CB985512

VERSION CB985512.1 GI:30280036

KEYWORDS

SOURCE EST.

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 781)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

Email: c9abbs@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

cDNA Library Preparation: CLONTech Laboratories, Inc.

cDNA Library Arrayed By: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: MDCh136 row: m column: 22

High quality sequence stop: 330.

Location/Qualifiers

1..781

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:30327573"

/lab_host="DH10B (TI phage-resistant)"

/clone_lib="NIH MGC 184"

/note="Organ: Pooled-glandular; Vector: pDNR-LIB; Site_1:

sffi (ggccattatggcc); Site 2: sffi (ggccgctggcc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGGCGCATATGAGC-3' and 3' adaptor sequence:
5'-ATCTAGAGCCGAGCGCCGACATG-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 72.6%; Score 233; DB 6; Length 781;
Best Local Similarity 82.9%; Pred. No. 4.2e-64;
Matches 266; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTCATCTGTAGAGACAGAGTCACC 60
DB 89 GACATCAAGATGACCCAGTCTCCATCTCCCTGTCATCTGTAGAGACAGAGTCACC 148
QY 61 ATCACTTGGCGGCGAGTCAAGCATTAGAGCCTATTAAATTGTATCAGAGAAACCA 120
DB 149 ATCACTTGGCGGCGAGTCAAGCATTAGAGCCTATTAAATTGTATCAGAGAAACCA 208
QY 121 GGAACGCTCTTAAGTCTCATTTAAGTGGCATCTACCCGGAAATCCGGGTCCTGAC 180
DB 209 GGGAAAGCCCTTAAGTCTCATTTAAGTGGCATCTACCCGGAAATCCGGGTCCTGAC 268
QY 181 CATTAGAGGCGGAGTGAATCTGGAGCAAAATTACATCTCCAGCAGCCCTGAGCCCT 240
DB 269 AGGTAGAGGCGGAGTGAATCTGGAGCAAAATTACATCTCCAGCAGCCCTGAGCCCT 328
QY 241 GAAGATTTTGTCTACTTACTTTGTCAAAGTCTGACAGTTGGCCATCCTTCGGCCAA 300
DB 329 GAAGATTTTGTCTACTTACTTTGTCAAAGTCTGACAGTTGGCCATCCTTCGGCCAA 388
QY 301 GGGACACGACTGGACATTCAA 321
DB 389 GGGACACGACTGGACATTCAA 409

RESULT 8
CD705041 553 bp mRNA linear EST 25-JUN-2003
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

CD705041 553 bp mRNA linear EST 25-JUN-2003
EST21568 human nasopharynx Homo sapiens cDNA, mRNA sequence.
CD705041
CD705041.1 GI:32235671
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 553)
Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
Transcriptional Gene Expression Profile of Human Nasopharynx
Unpublished (2003)
Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@zsums.edu.cn.
location/Qualifiers
1..553
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"

/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN

Query Match 72.1%; Score 231.6; DB 6; Length 553;
Best Local Similarity 83.0%; Pred. No. 1.1e-63;
Matches 264; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTCATCTGTAGAGACAGAGTCACC 60
DB 123 GACATCAAGATGACCCAGTCTCCATCTCCCTGTCATCTGTAGAGACAGAGTCACC 182
QY 61 ATCACTTGGCGGCGAGTCAAGCATTAGAGCCTATTAAATTGTATCAGAGAAACCA 120
DB 183 ATCACTTGGCGGCGAGTCAAGCATTAGAGCCTATTAAATTGTATCAGAGAAACCA 242
QY 121 GGAACGCTCTTAAGTCTCATTTAAGTGGCATCTACCCGGAAATCCGGGTCCTGAC 180
DB 243 GGGAAAGCCCTTAAGTCTCATTTAAGTGGCATCTACCCGGAAATCCGGGTCCTGAC 302
QY 181 CATTAGAGGCGGAGTGAATCTGGAGCAAAATTACATCTCCAGCAGCCCTGAGCCCT 240
DB 303 AGGTAGAGGCGGAGTGAATCTGGAGCAAAATTACATCTCCAGCAGCCCTGAGCCCT 362
QY 241 GAAGATTTTGTCTACTTACTTTGTCAAAGTCTGACAGTTGGCCATCCTTCGGCCAA 300
DB 363 GAAGATTTTGTCTACTTACTTTGTCAAAGTCTGACAGTTGGCCATCCTTCGGCCAA 422
QY 301 GGGACACGACTGGACATTC 318
DB 423 GGGACACGACTGGACATTC 440

RESULT 9
AM406227 421 bp mRNA linear EST 16-FEB-2000
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

AM406227 421 bp mRNA linear EST 16-FEB-2000
UI-HR-BU0-8CP-C-08-0-UI-r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3059726 5', mRNA sequence.
AM406227
AM406227.1 GI:6925284
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 421)
NIH-MGC <http://img.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNI at:
www.bio.lnl.gov/bdrp/image/image.html
Seq primer: M13 Forward.
location/Qualifiers
1..421
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="IMAGE:3059726"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC 37"
/note="Vector: pTR73-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA"

ORIGIN

(1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

Query Match 72.1%; Score 231.4; DB 2; Length 421;
Best Local Similarity 82.6%; Pred. No. 1.1e-63;
Matches 265; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTGATCTGTAGAGACAGATCAC 60
10 GACATCCAGATGACCCAGTCTCCATCTCCCTGCTGATCTGTAGAGACAGATCAC 69
61 ATCACTTCCGGGCGAGTCAAGATGACATTAAGCTATTAAATTGGTATGAGAAACA 120
70 ATCACTTCCGGGCGAGTCAAGATGACATTAAGCTATTAAATTGGTATGAGAAACA 129
121 GAGACAGCTCTTAAGCTGCTCAATTAAGCTGAGATCAACCGGGAATCCGGGGTCCCTGAC 180
130 GAGACAGCTCTTAAGCTGCTCAATTAAGCTGAGATCAACCGGGAATCCGGGGTCCCTGAC 189
181 CGATTACAGCGGCGAGTGAATCTGGGACAAATTACACTCTGACATCAGACGCTGACGCT 240
190 AGGTTCAAGCGGCGAGTGAATCTGGGACAAATTACACTCTGACATCAGACGCTGACGCT 249
241 GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCCATCCTTGGCCCA 300
250 GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCCATCCTTGGCCCA 309
301 GGGACAGCAGCTGACATTCAA 321
310 GGGACAGCAGCTGACATTCAA 330

RESULT 10
AM407904 422 bp mRNA linear EST 16-FEB-2000
LOCUS
DEFINITION
UT-HF-BL0-add-a-01-0-UI-F2 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3061128 5', mRNA sequence.
AM407904
AM407904.1 GI:6926961

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 422)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.lnl.gov/bdrp/image/image.html
Seq primer: M13 Forward.

FEATURES
source
1..422
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3061128"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_id="NIH_MGC_37"
/note="Vector: pT73-Pac; site_1: NotI; site_2: Eco RI;

ORIGIN

Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

Query Match 72.1%; Score 231.4; DB 2; Length 422;
Best Local Similarity 82.6%; Pred. No. 1.1e-63;
Matches 265; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTGATCTGTAGAGACAGATCAC 60
23 GACATCCAGATGACCCAGTCTCCATCTCCCTGCTGATCTGTAGAGACAGATCAC 82
61 ATCACTTCCGGGCGAGTCAAGATGACATTAAGCTATTAAATTGGTATGAGAAACA 120
83 ATCACTTCCGGGCGAGTCAAGATGACATTAAGCTATTAAATTGGTATGAGAAACA 142
121 GAGACAGCTCTTAAGCTGCTCAATTAAGCTGAGATCAACCGGGAATCCGGGGTCCCTGAC 180
143 GAGACAGCTCTTAAGCTGCTCAATTAAGCTGAGATCAACCGGGAATCCGGGGTCCCTGAC 202
181 CGATTACAGCGGCGAGTGAATCTGGGACAAATTACACTCTGACATCAGACGCTGACGCT 240
203 AGGTTCAAGCGGCGAGTGAATCTGGGACAAATTACACTCTGACATCAGACGCTGACGCT 262
241 GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCCATCCTTGGCCCA 300
263 GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCCATCCTTGGCCCA 322
301 GGGACAGCAGCTGACATTCAA 321
323 GGGACAGCAGCTGACATTCAA 343

RESULT 11
CD707755 521 bp mRNA linear EST 25-JUN-2003
LOCUS
DEFINITION
EST74282 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 521)
Liu,X.-Q., Zhou,Y., Zhang,L.-Y., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
Transcriptional Gene Expression Profile of Human Nasopharynx
Unpublished (2003)
Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 DongFeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.

FEATURES
source
1..521
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_id="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN

Query Match 72.1%; Score 231.4; DB 6; Length 521;
Best Local Similarity 82.6%; Pred. No. 1.2e-63;
Matches 265; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1 GAGCTCAGATGACCCAGTCTCATCTCCCTGCTGATCTGTAGAGACAGAGTCACC 60
DB 91 GACATCCAGATGACCCAGTCTCATCTCCCTGCTGATCTGTAGAGACAGAGTCACC 150
QY 61 ATCACTTGGCCGGGCAAGTCAAGACATTTAGAGCTATTTAATTGATATGACAGAAACCA 120
DB 151 ATCACTTGGCCAGGCGAGTCAAGACATTTAATTTAATTGATATGACAGAAACCA 210
QY 121 GGAACAGCTCTTAACTGCTCATTTTACTGGGCACTTACCCGGAAATCCGGGGTCCCTGAC 180
DB 211 GGGAAAGCCCCCTTAAGTCTCCATCTCAATGATCCATTTTGGAAACAGGGGTCTCATCA 270
QY 181 CGATTGAGGGGCGAGTGAATCTGGGACAAATTACATCTGACCATCGACAGCCGACCT 240
DB 271 AGGTTGAGTGAAGTGAATCTGGGACAGATTTTACTTTCACATCCACAGCCTGACGCT 330
QY 241 GAAGATTTTGGCTTACTTCTTTGTCACAGCTGACAGTTGGCCGATCACTTGGCCAA 300
DB 331 GAAGATTTTGCACATATTTACTGTCAACAGTTGATATCTCCGATCACCTTGGCCAA 390
QY 301 GGGACACGACTGGACATTTCA 321
DB 391 GGGACACGACTGGAGATTAA 411

RESULT 12
LOCUS BG756289 587 bp mRNA linear EST 15-MAY-2001
DEFINITION 602713607F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853953 5',
mRNA sequence.
ACCESSION BG756289
VERSION BG756289.1 GI:14066942
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 587)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LNCM1700 row: n column: 02
High quality sequence stop: 586.
Location/Qualifiers
1..587
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4853953"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site: 1; XhoI;
Site: 2; EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 72.1%; Score 231.4; DB 4; Length 587;

Best Local Similarity 82.6%; Pred. No. 1,3e-63;
Matches 265; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
QY 1 GAGCTCAGATGACCCAGTCTCATCTCCCTGCTGATCTGTAGAGACAGAGTCACC 60
DB 77 GACATCCAGATGACCCAGTCTCATCTCCCTGCTGATCTGTAGAGACAGAGTCACC 136
QY 61 ATCACTTGGCCGGGCAAGTCAAGACATTTAGAGCTATTTAATTGATATGACAGAAACCA 120
DB 137 ATCACTTGGCCAGGCGAGTCAAGATTTAATTTAATTGATATGACAGAAACCA 196
QY 121 GGAACAGCTCTTAACTGCTCATTTTACTGGGCACTTACCCGGAAATCCGGGGTCCCTGAC 180
DB 197 GGGAAAGCCCCCTTAAGTCTCCATCTCAATGATCCATTTTGGAAATAGGGGTCCCATCA 256
QY 181 CGATTGAGGGGCGAGTGAATCTGGGACAAATTACATCTGACCATCGACAGCCGACCT 240
DB 257 AGGTTGAGTGAAGTGAATCTGGGACAGATTTTACTTTCACATCGACAGCCTGACGCT 316
QY 241 GAAGATTTTGGCTTACTTCTTTGTCACAGCTGACAGTTGGCCGATCACTTGGCCAA 300
DB 317 GAAGATTTTGCACATATTTACTGTCAACGCGATGATATGCTCCGATCACCTTGGCCAA 376
QY 301 GGGACACGACTGGACATTTCA 321
DB 377 GGGACACGACTGGAAATTAA 397

RESULT 13
LOCUS CD690145 624 bp mRNA linear EST 25-JUN-2003
DEFINITION EST6668 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD690145
VERSION CD690145.1 GI:32210615
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 624)
Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and
Zeng, Y.-X.
Transcriptional Gene Expression Profile of Human Nasopharynx
Unpublished (2003)
Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
Location/Qualifiers
1..624
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN
Query Match 72.1%; Score 231.4; DB 6; Length 624;
Best Local Similarity 82.6%; Pred. No. 1.3e-63;
Matches 265; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
QY 1 GAGCTCAGATGACCCAGTCTCATCTCCCTGCTGATCTGTAGAGACAGAGTCACC 60
DB 114 GACATCCAGATGACCCAGTCTCATCTCCCTGCTGATCTGTAGAGACAGAGTCACC 173
QY 61 ATCACTTGGCCGGGCAAGTCAAGACATTTAGAGCTATTTAATTGATATGACAGAAACCA 120
DB 174 ATCACTTGGCCGGGCAAGTCAAGACATTTAGAGCTATTTAATTGATATGACAGAAACCA 233

QY 121 GACAGCCTCTTAAGCTGCTCATTTA CTGGGACATTACCGGGAATCCGGGGTCCCTGAC 180
DB 234 GGGAAAGCCCTTGAAGCTCTGATCTATGCTGATCAATTCAGTTGGCAAGTGGGATCCCATATA 293
QY 181 CGATTGAGCGGAGTGAATCTGGACAAATTACACTTCACATCAGACAGCTCGAGCCT 240
DB 294 AGATTGAGTGGAGTGGATCTGGGACAGATTTCACCTCAGCATCAGAGTCTGCAACCT 353
QY 241 GAAGATTTTGTCTACTTACTTTTGTCAACAGTCTGACAGATTGGCCGATCAGCTTCGGCCAA 300
DB 354 GAAGATTTTGTCAACTTACTTACTTCAACAGATTGACAGTTCAGTACCCTTGTGGCCAG 413
QY 301 GGGACACGACTGGACATTCGA 321
DB 414 GGGACCAAGCTGGAGATCAAA 434

RESULT 14
BG536784 570 bp mRNA linear EST 03-APR-2001
LOCUS 602566318F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4690877 5',
DEFINITION mRNA sequence.

ACCESSION BG536784
VERSION BG536784
KEYWORDS GI:13528330
SOURCE EST.
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL 1 (bases 1 to 570)
COMMENT Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: LHCMI509 row: c column: 06
High quality sequence stop: 568.

FEATURES
source location/Qualifiers
1..570
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4690877"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_77"
/note="Organ: Lung; Vector: pDNR-LIB (Clontech); Site: 1;
Site1 (ggcgccctcgagc); Site 2: Site1 (ggcgccatcgagc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGAGC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGGAGCGGCGGACGACG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 71.8%; Score 230.6; DB 4; Length 570;
Best Local Similarity 84.4%; Pred. No. 2.3e-63;
Matches 271; Conservative 0; Mismatches 49; Indels 1; Gaps 1;
QY 1 GAGCTCCAGATGACCGAGTCTCATCTCCCTGTCGATCTGTAGAGACAGATCACC 60
DB 91 GACATCCAGATGACCGAGTCTCATCTCCCTGTCGATCTGTGTGAGACAGATCACC 150

QY 61 ATCACTGCGCGGAGCAAGTCAAGACATTAAGACATTAATTAATGGTATCAGAGAAACA 120
DB 151 GTCACTTCCCGGCGGAGTCAAGACATTAAGACATTAATTAATGGTATCAGAGAAACA 210
QY 121 GGAAGCCTCTTAAGCTGCTCATTTTACTGGGCACTTACCCGGGAATCCGGGGTCCCTGAC 180
DB 211 GGAAGGCC-CTTAAGCCTCTGATTTTATGTTGATCATTGGCAAGTGGGGTCCCATCA 269
QY 181 CGATTGAGCGGAGGAAATCTGGGACAAATTACATCTCACCATCAGACAGCTGAGCCT 240
DB 270 AGTTTCAAGTGGAGAGATCTGGGACAAATTACATCTCACCATCAGAGTGTGCAACT 329
QY 241 GAAGATTTTGTCTACTTACTTTTGTCAACAGTCTGACAGTTTGGCCGATCAGCTTCGGCCAA 300
DB 330 GAAGATTTTGTCAACTTACTTACTTCAACAGATTCATATATCCGATCAGCTTCGGCCAA 389
QY 301 GGGACACGACTGGACATTCGA 321
DB 390 GGGACACGACTGGAGATTAAA 410

RESULT 15
CD683960 486 bp mRNA linear EST 25-JUN-2003
LOCUS CD683960
DEFINITION EST480 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD683960
VERSION CD683960.1 GI:32198500
KEYWORDS EST.
SOURCE EST.
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL 1 (bases 1 to 486)
COMMENT Unpublished (2003)

CONTACT: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.

FEATURES
source location/Qualifiers
1..486
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN

Query Match 71.6%; Score 229.8; DB 6; Length 486;
Best Local Similarity 82.2%; Pred. No. 3.9e-63;
Matches 264; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
QY 1 GAGCTCCAGATGACCGAGTCTCATCTCCCTGTCGATCTGTGAGACAGATCACC 60
DB 134 GACATCCAGATGACCGAGTCTCATCTCCCTGTCGATCTGTGAGACAGATCACC 193
QY 61 ATCACTGCGCGGAGCAAGTCAAGACATTAAGACATTAATTAATGGTATCAGAGAAACA 120
DB 194 ATCACTTGTGGGCGGAGTCAAGACATTAAGACATTAATTAATGGTATCAGAGAAACA 253
QY 121 GGAAGCCTCTTAAGCTGCTCATTTTACTGGGCACTTACCCGGGAATCCGGGGTCCCTGAC 180
DB 254 GGAAGGCCCTTAAGCTGCTCATTTTACTGGGCACTTACCCGGGAATCCGGGGTCCCATCA 313
QY 181 CGATTGAGCGGAGGAAATCTGGGACAAATTACATCTCACCATCAGACAGCTGAGCCT 240

Db	314	AGGTCAGCGCGCAGTGATCTGGGACAAATTCACCTCTACACATCAGCAGCCTGCAGCCT	373
QY	241	GAGGATTTTCTTACTTACTTTTGTCAACAGCTGACAGTTTGCCGATCACCCTTGCGCCAA	300
Db	374	GAGGATTTTGCACCTTATTTGTCAACAGGTAACAGGTTCCCGATCACCTTCGGCCAA	433
QY	301	GGGACACGACTGGACATTCAA	321
Db	434	GGGACACGACTGGAGATTAA	454

Search completed: December 7, 2004, 11:13:52
 Job time : 1875.31 secs



A DOCPHOENIX

APPL PARTS

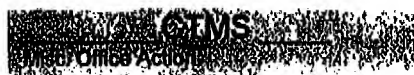


371P
 PCT Papers in a 371 Application
A...
 Amendment Including Elections
ABST
 Abstract
ADS
 Application Data Sheet
AF/D
 Affidavit or Exhibit Received
APPENDIX
 Appendix
ARTIFACT
 Artifact
BIB
 Bib Data Sheet
CLM
 Claim
COMPUTER
 Computer Program Listing
CRFL
 All CRF Papers for Backfile
DIST
 Terminal Disclaimer Filed
DRW
 Drawings
FOR
 Foreign Reference
FRPR
 Foreign Priority Papers
IDS
 IDS Including 1449

NPL
 Non-Patent Literature
OATH
 Oath or Declaration
PET
 Petition
RETMAIL
 Mail Returned by USPS
SEQLIST
 Sequence Listing
SPEC
 Specification
SPEC NO
 Specification Not in English
TRNA
 Transmittal New Application

CTNF
 Count Non-Final
CTRS
 Count Restriction
EXIN
 Examiner Interview
M903
 DO/EO Acceptance
M905
 DO/EO Missing Requirement
NFDR
 Formal Drawing Required
NOA
 Notice of Allowance
PETDEC
 Petition Decision

OUTGOING



1449
 Signed 1449
892
 892
ABN
 Abandonment
APDEC
 Board of Appeals Decision
APEA
 Examiner Answer
CTAV
 Count Advisory Action
CTEQ
 Count Ex parte Quayle
CTFR
 Count Final Rejection

INCOMING

AP.B
 Appeal Brief
C.AD
 Change of Address
N/AP
 Notice of Appeal
PA..
 Change in Power of Attorney
REM
 Applicant Remarks in Amendment
XT/
 Extension of Time filed separate

Internal

SRNT
 Examiner Search Notes
CLMPTO
 PTO Prepared Complete Claim Set

ECBOX
 Evidence Copy Box Identification
WCLM
 Claim Worksheet
WFEE
 Fee Worksheet

File Wrapper

FWCLM
 File Wrapper Claim
IIFW
 File Wrapper Issue Information
SRFW
 File Wrapper Search Info